

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 04:37:24 ; Search time 1684.26 Seconds
(without alignments)
7460.491 Million cell updates/sec

Title: US-09-852-261-1

Perfect score: 517

Sequence: 1 ggaccggagacgctctgcgg.....tgaaatacacaagtaaacat 517

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:
29: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
	1	344.2	66.6	796	14	CB959991
c	2	331.6	64.1	558	9	AI503976
c	3	330.6	63.9	673	12	BM984670
c	4	329.8	63.8	623	9	AW146128
c	5	326.6	63.2	575	9	AI248089
c	6	316.6	61.2	549	9	AI169253
c	7	315.8	61.1	558	9	AI265629
c	8	314.8	60.9	498	9	AA542914
	9	310	60.0	614	14	CD373004
	10	309	59.8	816	9	AI119218
	11	303.6	58.7	594	10	BF383724
c	12	299.8	58.0	527	9	AA913900
c	13	289.6	56.0	642	9	AI876493
c	14	287.4	55.6	499	9	AW495481
c	15	276	53.4	468	9	AI169770
	16	274.4	53.1	882	9	AI604642
c	17	268.2	51.9	430	9	AI478804
c	18	263.2	50.9	653	13	BQ200567
	19	258.4	50.0	608	9	AL599807
c	20	254.6	49.2	486	9	AA993659
c	21	254.2	49.2	521	9	AW493459
	22	254.2	49.2	559	12	BI715603
	23	254.2	49.2	602	13	BU590710
	24	254.2	49.2	621	12	BI221656
	25	254.2	49.2	1658	11	AK081019
	26	254	49.1	356	9	AW297586
c	27	253.2	49.0	595	9	AI573421
c	28	252.6	48.9	499	12	BI676839
c	29	252.6	48.9	500	9	AA945553
c	30	252.6	48.9	525	9	AA963258
	31	251.4	48.6	482	9	AA456717
c	32	251	48.5	706	9	AI401719
c	33	249.4	48.2	525	9	AI599751
	34	248.6	48.1	665	9	AA690767
	35	247.8	47.9	559	12	BI715465
	36	247.4	47.9	799	9	AI314558
c	37	247.2	47.8	499	12	BI294072
c	38	244.2	47.2	502	9	AI104669
c	39	243	47.0	561	12	BI714874
c	40	240.6	46.5	564	12	BI714981
	41	239.2	46.3	2170	11	AK038119
	42	237.4	45.9	558	12	BI715475
c	43	237.2	45.9	480	9	AA621551
	44	236.8	45.8	512	9	AI876203
	45	234.2	45.3	949	14	CB589117

ALIGNMENTS

RESULT 1
 CB959991
LOCUS CB959991 796 bp mRNA linear EST 29-APR-2003
DEFINITION AGENCOURT_13888044 NIH_MGC_147 Homo sapiens cDNA clone
 IMAGE:30341081 5', mRNA sequence.
ACCESSION CB959991
VERSION CB959991.1 GI:30216107
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 796)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDAM371 row: p column: 18
 High quality sequence stop: 707.
FEATURES
 source Location/Qualifiers
 1..796
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30341081"
 /tissue_type="Human Placenta"
 /lab_host="DH10B TonA"
 /clone_lib="NIH_MGC_147"
 /note="Organ: placenta; Vector: pBluescriptR; Site_1:
 ali-XhoI; Site_2: BamH; Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
 insert size 2.3 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIMH/NHGRI, National Institutes of Health). Note: This is
 a NIH_MGC library."
BASE COUNT 224 a 197 c 191 g 184 t
ORIGIN

Query Match 66.6%; Score 344.2; DB 14; Length 796;
 Best Local Similarity 87.3%; Pred. No. 8.3e-81;
 Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy 1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTCTCAGTCGTGTGGAGAC 60
 |||||||
 Db 180 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTCTCAGTCGTGTGGAGAC 239
 |||||||
 Qy 61 AGGGGTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG 120
 |||||||
 Db 240 AGGGGTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG 299
 |||||||
 Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
 |||||||
 Db 300 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 359
 |||||||
 Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
 |||||||
 Db 360 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 419
 |||||||
 Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
 |||||||
 Db 420 ATGCCCAAGACCCAG----- 434
 |||||||
 Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
 |||||||
 Db 435 ----AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 490
 |||||||
 Qy 361 GATGTA-GAAGACCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTGCTC 419
 |||||||
 Db 491 GATGTAGGAAGACCCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCCTTGCTC 550
 |||||||
 Qy 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC 477
 |||||||
 Db 551 TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTAA 610
 |||||||
 Qy 478 AAAGAT-GGCATTCCCCAATGAAATACACAAGTAAACAT 517
 |||||||
 Db 611 AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT 651

RESULT 2

AI503976/c

LOCUS AI503976 558 bp mRNA linear EST 11-MAR-1999
DEFINITION vm43d08.x1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA
 clone IMAGE:1001007 3' similar to gb:X04482 Mouse mRNA for
 preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION AI503976
VERSION AI503976.1 GI:4401827
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 558)
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,
 B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,
 E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Wilson,R.

TITLE The WashU-NCI Mouse EST Project 1999
 JOURNAL Unpublished
 COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:565223
 This clone was previously sequenced on the 5' end only, this new
 data is from the 3' end
 High quality sequence stop: 440.

FEATURES
 source Location/Qualifiers
 1..558
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:1001007"
 /tissue_type="diaphragm"
 /dev_stage="adult"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene mouse diaphragm (#937303)"
 /note="Organ: diaphragm; Vector: pBluescript SK-; Site_1:
 EcoRI; Site_2: XhoI; Cloned unidirectionally from mRNA
 prepared from diaphragm muscle. Primer: Oligo dT. Average
 insert size: 1.5 kb. Uni-ZAP XR Vector; ~5' adaptor
 sequence: 5' GAATTCTGGCACGAG 3' ~3' adaptor sequence: 5'
 CTCGAGTTTTTTTTTTTTTTTT 3'

BASE COUNT 103 a 133 c 149 g 173 t
 ORIGIN

Query Match 64.1%; Score 331.6; DB 9; Length 558;
 Best Local Similarity 82.0%; Pred. No. 1.7e-77;
 Matches 433; Conservative 0; Mismatches 84; Indels 11; Gaps 4;

Qy	1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGATGCTTCAGTCGTGTGGAGAC	60
Db	530 GGACCAGAGACCCTTGCGGGCTGAGCTGGATGCTTCAGTCGTGTGGACCG	471
Qy	61 AGGGGCTTTATTCACAACAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG	120
Db	470 AGGGGCTTTACTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG	411
Qy	121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	410 ACAGGCATTGTGGATGAGTGTTGCTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC	351
Qy	181 TGCGCACCCCTCAAGCCTGCCAACGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240
Db	350 TGTGCCCACTGAAGCCTACAAAGCAGCCGCTATCCGTGCCAGCGCCACACTGAC	291
Qy	241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G	297
Db	290 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG	231

Qy	298	AGAAGGAAAGGAAGTACATTGAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	357
Db	230	AGAAGGAAAGGAAGTACATTGAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA	171
Qy	358	CAGGATGTA-GAAGACCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTG	416
Db	170	CAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTG	111
Qy	417	CTCTGCACAGTTACCTGTAAACATTGAAATACCGGCCA-----AAAAATAAGTTGATC	470
Db	110	CTGCTTGAGCAACCTGCAAACATCGAAACACCTACCAAATAACAATAAGTCCAATA	51
Qy	471	ACATTCAAAAGAT-GGCATTCCCCAATGAAATAACACAAGTAAACAT	517
Db	50	ACATTACAAAGATGGGCATTCCCCAATGAAATAACACAAGTAAACAT	3

RESULT 3

BM984670/c

LOCUS BM984670 673 bp mRNA linear EST 20-FEB-2003
 DEFINITION UI-CF-EC1-abj-k-24-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
 UI-CF-EC1-abj-k-24-0-UI 3', mRNA sequence.
 ACCESSION BM984670
 VERSION BM984670.1 GI:19610417
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 673)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA=Yes.
 FEATURES Location/Qualifiers
 source 1. .673
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"

```
clone="UI-CF-EC1-abj-k-24-0-UI"
/tissue_type="Lung"
/dev_stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EC1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-EC1 is a normalized cDNA library containing the
following tissue(s): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
AAGTGCTTAC.
```

BASE COUNT 152 a 164 c 169 g 188 t
ORIGIN

Query Match 63.9%; Score 330.6; DB 12; Length 673;
Best Local Similarity 86.9%; Pred. No. 3.3e-77;
Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;

Qy 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGATGCTCTTCAGTTCTGTGTGGAGAC 60
|||||

Db 492 GGACCGGAGACCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTTGGAGAC 433

Qy 61 AGGGGCTTTATTCAA CAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTAG 120
||||| ||||| ||||| |||||

Db 432 AGGGG-TTTTATTTAGCAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 374

QY 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
||||| ||||| ||||| |||||

Db 373 ACAGGCATCGTGGATGAGTGTGCTGTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 314

DB 313 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTGTCCGTGCCAGGCCACACCGAC 254

Qy 241 ATGCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACCGAAGTCTCAGAGA 300
Ez |||||||

DB 253 ATGCCCAAGACCCAG----- 239

DB 238 ----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGAGGAAACAAGAACTACAG 183

Qy 361 GATGTA-GAAGACCCTCTGAGGAGTGAAGAAGGCACGCCACCGCAGGACCCCTTGCTC 419
||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||

Db 182 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC 123
 Qy 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC 477
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 122 TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTTA 63
 Qy 478 AAAGAT-GGCATTCCCCAATGAAATAACACAAGTAAACAT 517
 ||||| ||||| ||||| ||||| ||||| |||||
 Db 62 AAAGATGGCGTTTCCCCAATGAAATAACACAAGTAAACAT 22

RESULT 4

AW146128/c

LOCUS AW146128 623 bp mRNA linear EST 10-OCT-2000
DEFINITION um37e10.x1 Sugano mouse embryo mewa Mus musculus cDNA clone
 IMAGE:2247498 3' similar to gb:X04482 Mouse mRNA for
 preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION AW146128
VERSION AW146128.1 GI:6167864
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 623)
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
 ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
 ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Wilson,R.
TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished
COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:1006958
 Seq primer: custom primer used
 High quality sequence stop: 499.
FEATURES
source Location/Qualifiers
 1..623
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:2247498"
 /dev_stage="embryo, 14 dpc"
 /lab_host="DH10B"
 /clone_lib="Sugano mouse embryo mewa"
 /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
 Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
 with an oligo(dT) primer [ATGTGGCCTTTTTTTTT];
 double-stranded cDNA was ligated to a DraIII adaptor"

[TGTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XbaI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAGCTGCG and 3' end primer CGACCTGCAGCTGAGCACA."

BASE COUNT 123 a 138 c 170 g 191 t 1 others
ORIGIN

Query Match 63.8%; Score 329.8; DB 9; Length 623;
Best Local Similarity 80.6%; Pred. No. 5.3e-77;
Matches 425; Conservative 0; Mismatches 92; Indels 10; Gaps 3;

QY 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGAC 60

Qy 61 AGGGGGCTTTTATTTCAACAAGCCCCACAGGGTATGGCTCCAGCAGTCGGCACCCCCCTGCGAC 130

Db 481 AGGGGCTTTACTCAACAAGCCCACAGGCTATGGCTCCAGCATTGGAGGGCACCTCAG 422

QY 121 ACAGGCATCGGGATGAGTGTGCTTCGGAGCTGTATCTAAGGAGGCTGGAGATGTAT 180
 Ph 121 AGAGGCATTTCTGGATCTGATCTGCTTCGGAGCTGTATCTAAGGAGGCTGGAGATGTAT

Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTGTCCGTGCCAGGCCACACCGAC 240

Db 361 TGTGCCCACTGAAGCCTACAAAAGCAGCCGCTATCCGTGCCAGGCCACACTGAC 302

Db 301 ATGCCAAGACTCAGAACGTCCCCGTCCTATCGACAAACAAGAAAAACGAAGCTGCAAAGG 242

Qy 298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTCAGGAAACAAGAACTA 357

358 CAGGATGTA-GAAGACCTTCTGAGGAGTGAAGAAGGACAGGCCACCCGAGGACCCTTTC 416

Db 181 CAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTG 122

417 CTCGACAGTACCTGTAAACATTGGAAATACCGGCCA-----AAAAATAAGTTGATC 470
|| |
121 CTGCTTGAGCAACCTGCAAAGATCGAAAGCCGCTAACGATTAACGATTTCTCGATTC 66

Qy 471 ACATTTCAAAGATGGCATTTCCCCAATGAAATAACACAAGTAAACAT 517

DB 61 ACATTACAAAGATGGCATTTCCCCAATGAAATATACTAACAGTAAACAT 15

RESULT 5
AI248089/c
LOCUS AI248089 575 bp mRNA linear EST 01-DEC-1998
DEFINITION qh69f05.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA

clone IMAGE:1849953 3' similar to gb:X57025_rna1 INSULIN-LIKE
 GROWTH FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI248089
VERSION AI248089.1 GI:3843486
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 575)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 918 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 380.
FEATURES
source Location/Qualifiers
 1..575
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1849953"
 /sex="male"
 /dev_stage="20 week-post conception fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
 /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
 with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
 This is a subtracted version of the original Soares fetal
 liver spleen 1NFLS library. 1st strand cDNA was primed
 with a Pac I - oligo(dT) primer [5'
 AACTGGAAAGAATTAATTAAAGATCTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Pac I and cloned into the Pac I
 and Eco RI sites of the modified pT7T3 vector. Library
 went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 135 a 152 c 131 g 156 t 1 others
ORIGIN
 Query Match 63.2%; Score 326.6; DB 9; Length 575;
 Best Local Similarity 86.6%; Pred. No. 3.7e-76;
 Matches 438; Conservative 0; Mismatches 15; Indels 53; Gaps 5;
 Qy 16 TGCAGGGCTGAGCTGGTGATGCTCTTCAGTTCTGTGTGGAGACAGGGCTTTATTTC 75
 |||||||
 Db 551 TGCAGGGCTGAGCTGGTGATGCTCTTCAGTTCTGTGTGAAGACAGGGCTTTATTTC 492
 |||||||
 Qy 76 AACAAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAGACAGGCATCGTGGAT 135
 |||||||
 Db 491 AACAAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAGACAGGCATCGTGGAT 432

Qy 136 GAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAG 195
 |||||
 Db 431 GAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAG 372
 |||||
 Qy 196 CCTGCCAAGTCAGCTCGCTCTGCCAGCGCCACACCGACATGCCAAGACCCAG 255
 |||||
 Db 371 CCTGCCAAGTCAGCTCGCTCTGCCAGCGCCACACCGACATGCCAAGACCCAG 312
 |||||
 Qy 256 AAGTATCAGCCCCATCTACCAACAAGAACAGAAGTCTCAGAGAAGGAAAGGAAGTACA 315
 |||||
 Db 311 -----AAGGAAGTACA 301
 |||||
 Qy 316 TTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTA-GAAGACCC 374
 |||||
 Db 300 TTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGACCC 241
 |||||
 Qy 375 TTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTCTGCAC-AGTTACCTG 433
 |||||
 Db 240 TCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTCTGCACGAGTTACCTG 181
 |||||
 Qy 434 -TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTCAAAGAT-GGCATTTC 491
 |||||
 Db 180 TTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTAAAAGATGGCGTTTC 121
 |||||
 Qy 492 CCCCAATGAAATACACAAGTAAACAT 517
 |||||
 Db 120 CCCCAATGAAATACACAAGTAAACAT 95

RESULT 6

AI169253/c

LOCUS AI169253 549 bp mRNA linear EST 08-JAN-1999
DEFINITION EST215088 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone RKIBP33 3' end, mRNA sequence.
ACCESSION AI169253
VERSION AI169253.1 GI:4134375
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 549)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Gene Index
JOURNAL Unpublished
COMMENT On Oct 6, 1998 this sequence version replaced gi:3705561.
Other_ESTs: TC50779
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.

FEATURES Location/Qualifiers
 source 1..549
 /organism="Rattus sp."
 /mol_type="mRNA"
 /db_xref="taxon:10118"
 /clone="RKIBP33"
 /clone_lib="Normalized rat kidney, Bento Soares"
 /note="Organ: kidney; Vector: pT7T3Pac; Site_1: EcoRI;
 Site_2: NotI"

BASE COUNT 112 a 140 c 133 g 164 t
ORIGIN

Query Match 61.2%; Score 316.6; DB 9; Length 549;
 Best Local Similarity 80.8%; Pred. No. 1.7e-73;
 Matches 421; Conservative 0; Mismatches 89; Indels 11; Gaps 4;

Qy	8	AGACGCTCTGCAGGGCTGAGCTGGTGGATGCTCTCAGTCGTGTGGAGACAGGGCT	67
Db	549	AGACCCTTGCGGGCTGAGCTGGTGGACGCTCTCAATTGTGTGGACCAAGGGCT	490
Qy	68	TTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAGACAGGCA	127
Db	489	TTTACTCAACAAGCCCACAGGCTATGGCTCCAGCATTGAAGGGACCAACAGACGGCA	430
Qy	128	TGTTGGATGAGTGTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTATTGCGCAC	187
Db	429	TTGTGGATGAGTGTAGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCTC	370
Qy	188	CCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCGTGCCAGCGCCACACCGACATGCCA	247
Db	369	CGCTGAAGCCTACAAAGTCAGCTCGTCCATCCGGGCCAGCGCCACATTGACATGCCA	310
Qy	248	AGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---GAGAAGGA	304
Db	309	AGACTCAGAAGTCCCAGCCCCATCGACACACAAGAAAAGGAAGCTGCAAAGGAGAAGGA	250
Qy	305	AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATG	364
Db	249	AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACTTACAGAATG	190
Qy	365	TA-GAAGACCTTCTGAGGAGTGAAGAACAGGACAGGCCACCGCAGGACCCCTTGCTCTGCA	423
Db	189	TAGGAGGAGCCTCCGAGGAACAGAAAATGCCACGTACCGCAAGATCCTTGCTGCTTG	130
Qy	424	CAGTTACCTGTAAACATTGAAATACCGGCCA-----AAAAATAAGTTGATCACATTTC	477
Db	129	AGCAACCTGAAAACATCGGAACACCTGCCAATATCAATAATGAGTTCAATACCATTTC	70
Qy	478	AAAGAT-GGCATTCCCCAATGAAATACACAAGTAAACAT	517
Db	69	AGAGATGGCATTCCCTCAATGAAATACACAAGTAAACAT	29

RESULT 7
AI265629/c
LOCUS AI265629 558 bp mRNA linear EST 18-NOV-1998
DEFINITION uj04b07.x1 Sugano mouse liver mRNA Mus musculus cDNA clone

IMAGE:1890901 3' similar to gb:X04482 Mouse mRNA for
preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION AI265629
VERSION AI265629.1 GI:3883787
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 558)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:975225
Seq primer: custom primer used
High quality sequence stop: 495.
FEATURES Location/Qualifiers
source 1..558
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1890901"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACAC."
BASE COUNT 106 a 135 c 156 g 161 t
ORIGIN

Query Match 61.1%; Score 315.8; DB 9; Length 558;

Best Local Similarity 80.8%; Pred. No. 2.7e-73;
 Matches 408; Conservative 0; Mismatches 87; Indels 10; Gaps 3;

Qy	1	GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTCTTCAGTCGTGTGGAGAC	60
Db	506	GGACCAGAGACCCTTGCGGGCTGAGCTGGTGGATGCTCTTCAGTCGTGTGGACCG	447
Qy	61	AGGGGCTTTATTCAACAAGCCCACAGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG	120
Db	446	AGGGGCTTTACTTCAACAAGCCCACAGGTATGGCTCCAGCATTGGAGGGCACCTCAG	387
Qy	121	ACAGGCATCGTGGATGAGTGTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	386	ACAGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC	327
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCGTGCCAGCGCCACACCGAC	240
Db	326	TGTGCCCACTGAAGCCTACAAAAGCAGCCGCTATCCGTGCCAGCGCCACACTGAC	267
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G	297
Db	266	ATGCCCAAGACTCAGAAGTCCCCGTCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG	207
Qy	298	AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	357
Db	206	AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA	147
Qy	358	CAGGATGTA-GAAGACCTTCTGAGGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG	416
Db	146	CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTG	87
Qy	417	CTCTGCACAGTTACCTGTAAACATTGGAATACCGCCA-----AAAAATAAGTTGATC	470
Db	86	CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAAGTCCAATA	27
Qy	471	ACATTCAAAGATGGCATTCCCCC	495
Db	26	ACATTCAAAGATGGCATTCCCCC	2

RESULT 8
 AA542914/c
 LOCUS AA542914 498 bp mRNA linear EST 19-AUG-1997
 DEFINITION ni98c10.s1 NCI_CGAP_Pr21 Homo sapiens cDNA clone IMAGE:984882 3'
 similar to gb:X57025_rna1 INSULIN-LIKE GROWTH FACTOR IA PRECURSOR
 (HUMAN);, mRNA sequence.
 ACCESSION AA542914
 VERSION AA542914.1 GI:2291394
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 498)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 603 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 412.

FEATURES Location/Qualifiers
source 1..498
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:984882"
/sex="male"
/tissue_type="normal prostate"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr21"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 105 a 135 c 123 g 135 t
ORIGIN

Query Match 60.9%; Score 314.8; DB 9; Length 498;
Best Local Similarity 86.2%; Pred. No. 4.9e-73;
Matches 450; Conservative 0; Mismatches 17; Indels 55; Gaps 7;

Qy 1 GGACCGGAGACGCTCTGCGGGC-TGAGCTGGTGGATGCTCTTCAGTTCTGTGTGGAGA 59
Db 476 GGACCGGAGAACTTTGCAGGGCTTGAGCTGGTGGATGCTCTTCAGTTCTGTGTGGAGA 417

Qy 60 CAGGGCTTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCA 119
Db 416 CAGGGC-TTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCA 358

Qy 120 GACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTA 179
Db 357 GACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTA 298

Qy 180 TTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCTGCCAGCGCCACACCGA 239
Db 297 TTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCTGCCAGCGCCACACCGA 238

Qy 240 CATGCCAACAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAG 299

Db 237 CATGCCAAGACCCAG----- 222
 Qy 300 AAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTCAGGAAACAAGAACTACA 359
 |||||
 Db 221 ----AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTCAGGAAACAAGAACTACA 167
 |||||
 Qy 360 GGATGTA-GAAGACCCCTCTGAGGAGTGAAGAAGGCACGCCACCGCAGGACCCCTTGCT 418
 |||||
 Db 166 GGATGTAGGAAGACCCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCT 107
 |||||
 Qy 419 CTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATT 476
 |||||
 Db 106 CTGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATT 47
 |||||
 Qy 477 CAAAGAT-GGCATTCCCCAATGAAATACACAAGTAAACAT 517
 |||||
 Db 46 AAAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT 5

RESULT 9

CD373004

LOCUS CD373004 614 bp mRNA linear EST 29-MAY-2003
DEFINITION UI-R-GR0-csv-j-17-0-UI.r1 UI-R-GR0 Rattus norvegicus cDNA clone
 UI-R-GR0-csv-j-17-0-UI 5', mRNA sequence.
ACCESSION CD373004
VERSION CD373004.1 GI:31157094
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
REFERENCE 1 (bases 1 to 614)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 Tissue Procurement: James Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/rat.html>
 Seq primer: M13 REVERSE.
FEATURES
source Location/Qualifiers
 1. .614
 /organism="Rattus norvegicus"
 /mol_type="mRNA"

/strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-GR0-csv-j-17-0-UI"
 /tissue_type="Whole embryo"
 /dev_stage="embryo 13dpc"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-R-GR0"
 /note="Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I;
 UI-R-GR0 is a cDNA library containing the following
 tissue(s): rat whole embryo 13dpc. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. Denatured RNA was size
 fractionated on a 1% agarose gel. First strand cDNA
 synthesis was primed with oligo-dT primer containing a Not
 I site. Double strand cDNA was size selected according to
 mRNA size fraction, ligated with EcoR I adaptor, digested
 with NotI and then cloned directionally into pYX-Asc
 vector. The library tag sequence located between the Not I
 site and the polyA tail is CATCTCTACT. This library was
 created for the University of Iowa Program for Rat Gene
 Discovery and Mapping (Val Sheffield, Bento Soares and Tom
 Casavant)."

BASE COUNT 171 a 168 c 154 g 119 t 2 others
 ORIGIN

Query Match 60.0%; Score 310; DB 14; Length 614;
 Best Local Similarity 80.3%; Pred. No. 9.9e-72;
 Matches 388; Conservative 0; Mismatches 91; Indels 4; Gaps 2;

Qy	1	GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC	60
Db	116	GGACCAGAGACCCTTGCGGGCTGAGCTGGTGGACGCTTCAGTCGTGTGGACCA	175
Qy	61	AGGGGTTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCCCTCAG	120
Db	176	AGGGGTTTTACTCAACAAGCCCACAGGCTATGGCTCCAGCATTGGAGGGACCAACAG	235
Qy	121	ACAGGCATCGTGGATGAGTGTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	236	ACGGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	295
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCGTGCCAGCGCACACCGAC	240
Db	296	TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTCCATCCGGGCCAGCGCACACTGAC	355
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G	297
Db	356	ATGCCCAAGACTCAGAAGTCCCAGCCCCATCGACACACAAGAAAAGGAAGCTGCAAAGG	415
Qy	298	AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	357
Db	416	AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA	475
Qy	358	CAGGATGTA-GAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTG	416
Db	476	CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATTCCACGTCACCGCATGATCCTTG	535

Qy	417	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTT	476
Db	536	CTGCTTGAGCAACCTGCANAACATCGAACACCTGCCAATATCAATAATGAGTTCAATA	595
Qy	477	CAA 479	
		.	
Db	596	CCA 598	

RESULT 10

AII19218

LOCUS AI119218 816 bp mRNA linear EST 02-SEP-1998
 DEFINITION ue94h02.y1 Sugano mouse embryo mewa Mus musculus cDNA clone
 IMAGE:1498803 5' similar to gb:X04482 Mouse mRNA for
 preproinsulin-like growth factor IB (MOUSE) ; mRNA sequence.
 ACCESSION AI119218
 VERSION AI119218.1 GI:3519542
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 816)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 TITLE The WashU-HHMI Mouse EST Project
 JOURNAL Unpublished
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:936407
 Seq primer: custom primer used
 High quality sequence stop: 473.
 FEATURES Location/Qualifiers
 source 1. .816
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:1498803"
 /dev_stage="embryo, 14 dpc"
 /lab_host="DH10B"
 /clone_lib="Sugano mouse embryo mewa"
 /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
 Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
 with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTT];
 double-stranded cDNA was ligated to a DraIII adaptor
 [TGTTGGCCTACTGG], digested and cloned into distinct DraIII

sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XbaI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."

BASE COUNT 230 a 219 c 172 g 187 t 8 others
ORIGIN

Query Match 59.8%; Score 309; DB 9; Length 816;
Best Local Similarity 80.2%; Pred. No. 2e-71;
Matches 384; Conservative 0; Mismatches 91; Indels 4; Gaps 2;

Qy	1	GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC	60
Db	323		382
Qy	61	AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG	120
Db	383		442
Qy	121	ACAGGCATCGTGGATGAGTGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	443		502
Qy	181	TGCCCACCCCTCAAGCCTGCCAACGTCAGCTCGCTCTGTCCTGCCAGCGCCACACCGAC	240
Db	503		562
Qy	241	ATGCCAACAGCCCCAGAACAGTACAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G	297
Db	563		622
Qy	298	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	357
Db	623		682
Qy	358	CAGGATGTA-GAAGACCCCTCTGAGGAGTGAAGAACAGGCCACCGCAGGACCCCTTG	416
Db	683		742
Qy	417	CTCTGCACAGTTACCTGTAAACATTGAAATACCGGCCAAAAATAAGTTGATCACATT	475
Db	743		801

RESULT 11

BF383724

LOCUS BF383724 594 bp mRNA linear EST 27-NOV-2000
DEFINITION 602044632F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4194295 5',
mRNA sequence.
ACCESSION BF383724
VERSION BF383724.1 GI:11365029
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 594)

REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM9527 row: p column: 08
 High quality sequence stop: 589.

FEATURES source Location/Qualifiers
 . .594
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4194295"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Li9"
 /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.9 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 175 a 162 c 142 g 115 t
 ORIGIN

Query Match 58.7%; Score 303.6; DB 10; Length 594;
 Best Local Similarity 80.7%; Pred. No. 4.9e-70;
 Matches 394; Conservative 0; Mismatches 84; Indels 10; Gaps 3;

Qy	16	TGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCTGTGTGGAGACAGGGGCTTTATTTC	75
Db	107	TGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCTGTGTGGACCGAGGGGCTTTACTTC	166
Qy	76	AACAAGCCCACAGGGTATGGCTCCAGCAGTCGAGGGGCCCTCAGACAGGCATCGTGGAT	135
Db	167	AACAAGCCCACAGGTATGGCTCCAGCATTGGAGGGCACCTCAGACAGGCATTGTGGAT	226
Qy	136	GAGTGTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAG	195
Db	227	GAGTGTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTACTGTGCCCACTGAAG	286
Qy	196	CCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGACATGCCAAGACCCAG	255
Db	287	CCTACAAAAGCAGCCGCTCTATCCGTGCCAGCGCCACACTGACATGCCAAGACTCAG	346
Qy	256	AAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA--GAGAAGGAAAGGAAGT	312
Db	347	AAGTCCCCGTCCCTATCGACAAACAAGAAACGAAGCTGCAAAGGAGAAGGAAGT	406

RESULT 12

AA913900/c

LOCUS AA913900 527 bp mRNA linear EST 24-SEP-1998
 DEFINITION ol35g05.s2 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
 IMAGE:1525496 3' similar to gb:X57025_rna1 INSULIN-LIKE GROWTH
 FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.
 ACCESSION AA913900
 VERSION AA913900.1 GI:3053292
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 527)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 870 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 97.
 FEATURES Location/Qualifiers
 source 1. .527
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1525496"
 /lab_host="DH10B"
 /clone_lib="Soares_NFL_T_GBC_S1"
 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NbHL19W, testis NHT, and B-cell
 NCI_CGAP_GCB1) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as

tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 125 a 134 c 119 g 149 t
ORIGIN

Query Match 58.0%; Score 299.8; DB 9; Length 527;
Best Local Similarity 85.5%; Pred. No. 4.9e-69;
Matches 413; Conservative 0; Mismatches 17; Indels 53; Gaps 5;

Qy	39	TCTTCAGTCGTGTGGAGACAGGGGCTTTATTTACAACAAGCCCACAGGGTATGGCTC	98
Db	527	TCTTCAGTCGTGTGGAGACAGGGGCTTTATTTACAACAAGCCCACAGGGTATGGCTC	468
Qy	99	CAGCAGTCGGAGGGCGCCTCAGACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGA	158
Db	467	CAGCAGTCGGAGGGCGCCTAAGACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGA	408
Qy	159	TCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGT	218
Db	407	TCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGT	348
Qy	219	CCGTGCCAGGCCACACCGACATGCCAAGACCCAGAACAGTATCAGCCCCCATCTACCAA	278
Db	347	CCGTGCCAGGCCACACCGACATGCCAAGACCCAG-----	311
Qy	279	CAAGAACACGAAGTCTCAGAGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGA	338
Db	310	-----AAGGAAGTACATTGAAGAACGCAAGTAGAGGGA	277
Qy	339	GTGCAGGAAACAAGAACTACAGGATGTA-GAAGACCCCTCTGAGGAGTGAAGAAGGACAG	397
Db	276	GTGCAGGAAACAAGAACTACAGGATGTAGGAAGACCCCTCTGAGGAGTGAAGAGTGACAT	217
Qy	398	GCCACCGCAGGACCCTTGCTCTGCAC-AGTACCTG-TAAACATTGGAATACCGGCCAA	455
Db	216	GCCACCGCAGGATCCTTGCTCTGCACGAGTTACCTGTTAAACTTGGAACACCTACCAA	157
Qy	456	AAAATAAGTTGATCACATTCAAAGAT-GGCATTCCCCAATGAAATACACAAGTAAA	514
Db	156	AAAATAAGTTGATAACATTAAAAGATGGCGTTCCCCAATGAAATACACAAGTAAA	97
Qy	515	CAT 517	
Db	96	CAT 94	

RESULT 13

AI876493/c

LOCUS AI876493 642 bp mRNA linear EST 21-JUL-1999
DEFINITION uj59b10.x1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1924219 3' similar to gb:X57025_rna1 INSULIN-LIKE GROWTH
FACTOR IA PRECURSOR (HUMAN); gb:X04482 Mouse mRNA for
preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION AI876493
 VERSION AI876493.1 GI:5550542
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 642)
 AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
 ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
 ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Wilson,R.
 TITLE The WashU-NCI Mouse EST Project 1999
 JOURNAL Unpublished
 COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:980511
 Seq primer: custom primer used
 High quality sequence stop: 257.
 FEATURES Location/Qualifiers
 source 1. .642
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:1924219"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="Sugano mouse liver mlia"
 /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
 (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATGTGGCCTTTTTTTTTTT]; double-stranded cDNA was
 ligated to a DraIII adaptor [TGGTGGCCTACTGG], digested
 and cloned into distinct DraIII sites of the pME18S-FL3
 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
 be used to isolate the cDNA insert. Size selection was
 performed to exclude fragments <1.5kb. Library
 constructed by Dr. Sumio Sugano (University of Tokyo
 Institute of Medical Science). Custom primers for
 sequencing: 5' end primer CTTCTGCTCTAAAGCTGCG and 3' end
 primer CGACCTGCAGCTCGAGCACA."
 BASE COUNT 127 a 154 c 175 g 185 t 1 others
 ORIGIN

Query Match 56.0%; Score 289.6; DB 9; Length 642;
 Best Local Similarity 78.9%; Pred. No. 2.7e-66;
 Matches 397; Conservative 0; Mismatches 95; Indels 11; Gaps 4;

Qy 2 GACCGGAGACGCTCTGCCGGCTGAGCTGGATGCTTCAGTCGTGTGGAGACA 61
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 503 GACCAGAGACCCCTTGCGGGCTGAGCTGGTGGATGCTCTCAGGTCGTGTGGAGCGA 444
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 62 GGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAGA 121
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 443 GGGGCTTTCTCAACAAGGCCACAGGCTATGGCTCCAGCATTGGAGGGCACCTCAGA 384
 ||||| ||||| ||||| ||||| ||||| |||||
 Qy 122 CAGGCATCGTGGATGAGTGCTGCTTCGG-AGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 383 CAGTCAATGTGGATGAGTGTTGCTTCGGAACGCTGTGATCTGAGAAAGACTGNAGATGTAC 324
 ||||| ||||| ||||| ||||| |||||
 Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGGCCACACCGAC 240
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 323 TGTGCCCACTGAAGCCTACAAAAGCAGCCGCTATCCGTGCCAGGCCACACTGAC 264
 ||||| ||||| ||||| |||||
 Qy 241 ATGCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 263 ATGCCAAGACTCAGAAGTCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 204
 ||||| ||||| |||||
 Qy 298 AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 203 AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 144
 ||||| |||||
 Qy 358 CAGGATGTA-GAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTG 416
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 143 CAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTG 84
 ||||| |||||
 Qy 417 CTCTGCACAGTTACCTGTAACATTGGAATACCGGCCA-----AAAAATAAGTTGATC 470
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 83 CTGCTTGAGCAACCTGCAAACATCGAAACACTACCAAATAACAATAAGTCCAATA 24
 |||||
 Qy 471 ACATTCAAAGATGGCATTCCC 493
 ||||| ||||| ||||| |||||
 Db 23 ACATTCAAAGATGGCATTCCC 1

RESULT 14

AW495481/c

LOCUS AW495481 499 bp mRNA linear EST 24-FEB-2000
 DEFINITION UI-M-BH3-ayu-g-11-0-UI.s1 NIH_BMAP_M_S4 Mus musculus cDNA clone
 UI-M-BH3-ayu-g-11-0-UI 3', mRNA sequence.
 ACCESSION AW495481
 VERSION AW495481.1 GI:7065762
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 499)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: Chin, H

National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bona fide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized pineal glands library cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
Seq primer: M13 Forward
POLYA=Yes.

FEATURES	Location/Qualifiers
source	1. .499 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UI-M-BH3-ayu-g-11-0-UI" /dev_stage="27-32 days" /lab_host="DH10B (Life Technologies)" /clone_lib="NIH_BMAP_M_S4" /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S4 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S4, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1, NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library (NIH_BMAP_M_S4) was constructed as follows: PCR amplified cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996) TAG_LIB=NIH_BMAP_M_S4 TAG_TISSUE=pineal-glands

TAG_SEQ=CAGAC"

BASE COUNT 86 a 112 c 124 g 177 t
ORIGIN

Query Match 55.6%; Score 287.4; DB 9; Length 499;
Best Local Similarity 80.8%; Pred. No. 9.7e-66;
Matches 387; Conservative 0; Mismatches 81; Indels 11; Gaps 4;

Qy 50 TGTGTGGAGACAGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGA 109
Db 499 TGTGTGGACCGAGGGGCTTTACTCAACAAGCCCACAGGCTATGGCTCCAGCATTGGA 440

Qy 110 GGGCGCCTCAGACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGC 169
Db 439 GGGCACCTCAGACAGGCATTGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGAC 380

Qy 170 TGGAGATGTATTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTGTCCGTGCCAGC 229
Db 379 TGGAGATGTACTGTGCCCACTGAAGCCTACAAAAGCAGCCGCTATCGACAAACAAGAAAACGA 320

Qy 230 GCCACACCGACATGCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGA 289
Db 319 GCCACACTGACATGCCAAGACTCAGAAGTCCCGTCCCTATCGACAAACAAGAAAACGA 260

Qy 290 AGTCTCA---GAGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGA 346
Db 259 AGCTGCAAAGGAGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGAAGTGCAGGA 200

Qy 347 AACAAAGAACTACAGGATGTA-GAAGACCCTCTGAGGAGTGAAGAAGGACAGGCCACCGC 405
Db 199 AACAAAGACCTACAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCAC 140

Qy 406 AGGACCCTTGCTCTGCACAGTTACCTGTAAACATTGGAATACCGGCC----AAAAA 459
Db 139 AGGATCCTTGCTGCTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAA 80

Qy 460 TAAGTTGATCACATTCAAAGAT-GGCATTCCCCAATGAAATACACAAGTAAACAT 517
Db 79 TAAGTCCAATAACATTCAAAGATGGCATTTCCCCAATGAAATATAAGTAAACAT 21

RESULT 15

AI169770/c

LOCUS AI169770 468 bp mRNA linear EST 20-JAN-1999
DEFINITION EST215669 Normalized rat liver, Bento Soares Rattus sp. cDNA clone
RLIAT07 3' end, mRNA sequence.
ACCESSION AI169770
VERSION AI169770.1 GI:3709810
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 468)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.

Db

48 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ATTCAGAGATGGGCATTCCTCAATGAAATACACAAGTAAACAT 3

Search completed: December 13, 2003, 07:29:47
Job time : 1690.26 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 05:41:20 ; Search time 2309.97 Seconds
(without alignments)
9156.102 Million cell updates/sec

Title: US-09-852-261-1

Perfect score: 517

Sequence: 1 ggaccggagacgctctgcgg.....tgaaatacacaagtaaacat 517

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

```

28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	517	100.0	517	6	AX147742	AX147742 Sequence
2	517	100.0	517	6	AX300779	AX300779 Sequence
3	467.4	90.4	523	6	AX147746	AX147746 Sequence
4	467.4	90.4	523	6	AX300783	AX300783 Sequence
5	377.2	73.0	471	6	AX147754	AX147754 Sequence
6	377.2	73.0	471	6	AX300791	AX300791 Sequence
7	355.4	68.7	444	9	HSU40870	U40870 Human alter
8	344.2	66.6	616	9	HSIGF1A	X56773 H.sapiens m
9	344.2	66.6	7260	6	AX375028	AX375028 Sequence
10	344.2	66.6	7260	6	AX411095	AX411095 Sequence
11	344.2	66.6	7260	9	HSIGFACI	X57025 Human IGF-I
12	342.6	66.3	666	6	A29119	A29119 H.sapiens I
13	342.6	66.3	725	9	HSIGFI	X00173 Homo sapien
14	342.6	66.3	728	9	HUMGFI	M29644 Human insul
15	342.6	66.3	1076	9	HUMIGFI	M27544 Human insul
16	341	66.0	620	6	I08370	I08370 Sequence 2
17	331.6	64.1	1536	10	BC012409	BC012409 Mus muscu
18	330	63.8	798	10	RNIGFI2	X06108 Rat mRNA (c
19	330	63.8	958	10	RNIGFI1	X06107 Rat mRNA (c
20	326.8	63.2	710	10	RATIGFIA	M15480 Rat insulin
21	325.2	62.9	539	6	AX147744	AX147744 Sequence
22	325.2	62.9	539	6	AX300781	AX300781 Sequence
23	318.2	61.5	651	10	MMIGFIBR	X04482 Mouse mRNA
24	308.6	59.7	730	9	HSIGF1B	X56774 H.sapiens m
25	308.6	59.7	1094	9	HUMGFB	M11568 Human insul
26	308.6	59.7	1136	6	E01349	E01349 cDNA encodi
27	308.6	59.7	1136	6	I08009	I08009 Sequence 3
28	294.4	56.9	432	4	AF022961	AF022961 Oryctolag
29	286.4	55.4	3599	6	BD063790	BD063790 Insulin-1
30	286.4	55.4	3599	6	BD069041	BD069041 Treatment
31	286.4	55.4	3600	6	BD063789	BD063789 Insulin-1
32	286.4	55.4	3600	6	BD069040	BD069040 Treatment
33	285.4	55.2	612	9	HUMIGFIB	M37484 Human insul

34	283.4	54.8	888	4	ECU85272	U85272 Equus cabal
35	281.2	54.4	532	4	SSILGF1M	X17492 Porcine mRNA
36	281.2	54.4	567	4	PIGGFIIA	M31175 Pig insulin
37	276	53.4	1284	4	BTILGF1A	X15726 Bovine mRNA
38	271.2	52.5	978	4	GOTIGFI	D11378 Goat mRNA f
39	271.2	52.5	978	6	E05279	E05279 DNA encoding
40	267.6	51.8	836	10	CPIGF1	X52951 Guinea pig
41	264.8	51.2	747	4	SHPIGFIA6	M31735 Sheep insulin
42	264.8	51.2	790	4	SHPIGFIA21	M31734 Sheep insulin
43	264.8	51.2	1015	4	SHPIGFIA46	M31736 Sheep insulin
44	264.8	51.2	1107	4	SHPIGFIA1	M30653 Sheep insulin
45	258.4	50.0	317	6	AX147750	AX147750 Sequence

ALIGNMENTS

RESULT 1

AX147742

LOCUS AX147742 517 bp DNA linear PAT 31-AUG-2001
 DEFINITION Sequence 1 from Patent WO0136483.
 ACCESSION AX147742
 VERSION AX147742.1 GI:14346787
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Goldspink, G.R. and Johnson, I.R.
 TITLE Use of the insulin-like-growth factor i isoform mgf for the
 treatment of neurological disorders
 JOURNAL Patent: WO 0136483-A 1 25-MAY-2001;
 University College London (GB)
 FEATURES Location/Qualifiers
 source 1..517
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 CDS <1..333
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAC41175.1"
 /db_xref="GI:14346788"
 /db_xref="REMTREMBL: CAC41175"
 /translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSRRAPQTGIV
 DECCFRSCDLRRLEMYCAPLKAKSARSVAQRHTDMPKTQKYQPPSTNKNTKSQRKK
 GSTFEEHK"

BASE COUNT 150 a 130 c 139 g 98 t
 ORIGIN

Query Match 100.0%; Score 517; DB 6; Length 517;
 Best Local Similarity 100.0%; Pred. No. 4.4e-155;
 Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTTCAGTTCTGTGTGGAGAC 60
 |||||||

Db 1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGATGCTTCAGTTCGTGTGGAGAC 60
 Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 120
 |||||||
 Db 61 AGGGGCTTTATTCAACAAGCCCACAGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 120
 |||||||
 Qy 121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
 |||||||
 Db 121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
 |||||||
 Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGGCCAACCGAC 240
 |||||||
 Db 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGGCCAACCGAC 240
 |||||||
 Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
 |||||||
 Db 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
 |||||||
 Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
 |||||||
 Db 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
 |||||||
 Qy 361 GATGTAGAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTCT 420
 |||||||
 Db 361 GATGTAGAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTCT 420
 |||||||
 Qy 421 GCACAGTTACCTGTAAACATTGGAATACCGGCAAAAAATAAGTTGATCACATTCAAA 480
 |||||||
 Db 421 GCACAGTTACCTGTAAACATTGGAATACCGGCAAAAAATAAGTTGATCACATTCAAA 480
 |||||||
 Qy 481 GATGGCATTCCCCAATGAAATACACAAGTAAACAT 517
 |||||||
 Db 481 GATGGCATTCCCCAATGAAATACACAAGTAAACAT 517

RESULT 2

AX300779

LOCUS AX300779 517 bp DNA linear PAT 30-NOV-2001
 DEFINITION Sequence 1 from Patent WO0185781.
 ACCESSION AX300779
 VERSION AX300779.1 GI:17382060
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Goldspink, G.D. and Terenghi, G.B.
 TITLE Repair of nerve damage
 JOURNAL Patent: WO 0185781-A 1 15-NOV-2001;
 University College London (GB) ; East Grinstead Medical Research
 Trust (GB)
 FEATURES Location/Qualifiers
 source 1. .517
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

CDS <1..333
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD13040.1"
/db_xref="GI:17382061"
/translation="GPETLCGAEELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIV
DECCFRSCDLRRLEMYCAPLKA KSAR SVRAQRHTDMPKTQKYQPPSTNKNTKSQRK
GSTFEEHK"

BASE COUNT 150 a 130 c 139 g 98 t
ORIGIN

Query Match 100.0%; Score 517; DB 6; Length 517;
Best Local Similarity 100.0%; Pred. No. 4.4e-155;
Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 AGGGGCTTTATTCACAAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 120

31 AGGCTTTCAGATGCCACCACTCCACACTGGGAGGGGGCTCAG 120

Db 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Pb 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240

Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 301 AGGAAAGGAAGTACATTGAGAACACAAGTAGAGGGAGTCAGGAAACAAGAACTACAG 360

Qy 361 GATGTAGAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTCT 420

Db 361 GATGTAGAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTCT 420
QV 421 CGAGACTTACCTCTTAACTTGGATTCCTGGGGGTTTATTTTCTTCTTCTTCTTCTTCTTCTT

Db 421 GCACAGTTACCTGAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTCAAA 480

Db 481 GATGGCATTTCCCCAATGAAATAACACAAGTAAACAT 517

RESULT 3

AX147746

LOCUS AX147746 523 bp DNA linear PAT 31-AUG-2001

DEFINITION Sequence 5 from Patent WO0136483.

ACCESSION AX147746

VERSION AX147746.1 GI:14346791
 KEYWORDS
 SOURCE Oryctolagus cuniculus (rabbit)
 ORGANISM Oryctolagus cuniculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 REFERENCE 1
 AUTHORS Goldspink, G.R. and Johnson, I.R.
 TITLE Use of the insulin-like-growth factor i isoform mgf for the treatment of neurological disorders
 JOURNAL Patent: WO 0136483-A 5 25-MAY-2001;
 University College London (GB)
 FEATURES Location/Qualifiers
 source 1. .523
 /organism="Oryctolagus cuniculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:9986"
 CDS <1. .336
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAC41177.1"
 /db_xref="GI:14346792"
 /db_xref="REMTREMBL:CAC41177"
 /translation="GPETLCGAEVDALQFVCGDRGFYFNKPTGYGSSSRAPQTGIV
 DECCFRSCDLRRLEMYCAPLPAKAARSVRAQRHTDMPKTQKYQPPSTNKKMKSQR
 KGSTFEEHK"

BASE COUNT 154 a 129 c 142 g 98 t
 ORIGIN

Query Match 90.4%; Score 467.4; DB 6; Length 523;
 Best Local Similarity 96.2%; Pred. No. 4.4e-139;
 Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

Qy	1	GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTTCAGTTCTGTGTGGAGAC	60
Db	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTTCAGTTCTGTGTGGAGAC	60
Qy	61	AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG	120
Db	61	AGGGGCTTTATTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Qy	121	ACAGGCATCGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	121	ACAGGCATCGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCACACCGAC	240
Db	181	TGTGCACCCCTCAAGCCGAAAGGCAGCCGCTCCGTCCGTGCCAGCGCACACCGAC	240
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G	297
Db	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Qy	298	AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	357
Db	301	AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360

Qy 358 CAGGATGTA-GAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTG 416
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 361 CAGGATGTAGGAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTG 420
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Qy 417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTT 476
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTT 480
 ||||||| ||||||| ||||||| ||||||| |||||||
 Qy 477 CAAAGATGGCATTCCCCAATGAAATAACAAGTAAACAT 517
 ||||||| ||||||| ||||||| ||||||| |||||||
 Db 481 CAAAGATGGCATTCCCCAATGAAATAACAAGTAAACAT 521

RESULT 4

AX300783

LOCUS AX300783 523 bp DNA linear PAT 30-NOV-2001
 DEFINITION Sequence 5 from Patent WO0185781.
 ACCESSION AX300783
 VERSION AX300783.1 GI:17382064
 KEYWORDS
 SOURCE Oryctolagus cuniculus (rabbit)
 ORGANISM Oryctolagus cuniculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 REFERENCE 1
 AUTHORS Goldspink, G.D. and Terenghi, G.B.
 TITLE Repair of nerve damage
 JOURNAL Patent: WO 0185781-A 5 15-NOV-2001;
 University College London (GB) ; East Grinstead Medical Research
 Trust (GB)
 FEATURES Location/Qualifiers
 source 1. .523
 /organism="Oryctolagus cuniculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:9986"
 CDS <1. .336
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAD13042.1"
 /db_xref="GI:17382065"
 /translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRAPQTGIV
 DECCFRSCDLRLEMYPPLKAARSVRAQRHTDMPKTQKYQPPSTNKKMKSQRRR
 KGSTFEEHK"

BASE COUNT	154	a	129	c	142	g	98	t
ORIGIN								

Query Match 90.4%; Score 467.4; DB 6; Length 523;
 Best Local Similarity 96.2%; Pred. No. 4.4e-139;
 Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGGGGCTGAGCTGGTGGATGCTCTTCAGTCGTGTGGAGAC 60
 ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 1 GGACCGGAGACGCTCTGGGTGCTGAGCTGGTGGATGCTCTTCAGTCGTGTGGAGAC 60
 ||||||| ||||||| ||||||| ||||||| |||||||
 Qy 61 AGGGGCTTTATTCACAAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCCCTCAG 120
 ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 61 AGGGGCTTTATTCACAAAGCCCACAGGATAACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy 121 ACAGGCATCGGATGAGTGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
 |||||||
 Db 121 ACAGGCATCGGATGAGTGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
 |||||||
 Qy 181 TGGCACCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
 |||||||
 Db 181 TGTGCACCCTCAAGCCGGAAAGGCAGCCCCTCGTCCGTGCCAGCGCCACACCGAC 240
 |||||||
 Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
 |||||||
 Db 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
 |||||||
 Qy 298 AGAAGGAAAGGAAGTACATTGAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
 |||||||
 Db 301 AGAAGGAAAGGAAGTACATTGAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
 |||||||
 Qy 358 CAGGATGTA-GAAGACCCCTCTGAGGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTG 416
 |||||||
 Db 361 CAGGATGTAGGAAGACCCCTCTGAGGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTG 420
 |||||||
 Qy 417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATT 476
 |||||||
 Db 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATT 480
 |||||||
 Qy 477 CAAAGATGGCATTTCCCCAATGAAATACACAAGTAAACAT 517
 |||||||
 Db 481 CAAAGATGGCATTTCCCCAATGAAATACACAAGTAAACAT 521

RESULT 5

AX147754

LOCUS AX147754 471 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 13 from Patent WO0136483.
ACCESSION AX147754
VERSION AX147754.1 GI:14348552
KEYWORDS
SOURCE Oryctolagus cuniculus (rabbit)
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1
AUTHORS Goldspink, G.R. and Johnson, I.R.
TITLE Use of the insulin-like-growth factor i isoform mgf for the
treatment of neurological disorders
JOURNAL Patent: WO 0136483-A 13 25-MAY-2001;
University College London (GB)
FEATURES Location/Qualifiers
source 1. .471
/organism="Oryctolagus cuniculus"
/mol_type="genomic DNA"
/db_xref="taxon:9986"
CDS <1..318
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC41264.1"
/db_xref="GI:14348553"

/translation="GPETLCGAEVLVDALQFVCGDRGFYFNKPTGYGSSSRAPQTGIV
DECCFRSCDLRRLEMYCAPLKAARSVRAQRHTDMPKTQKEVHLKNTSRGSAGNKN
YRM"

BASE COUNT 132 a 118 c 131 g 90 t
ORIGIN

Query Match 73.0%; Score 377.2; DB 6; Length 471;
Best Local Similarity 87.8%; Pred. No. 5.4e-110;
Matches 455; Conservative 0; Mismatches 13; Indels 50; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGCCGGCTGAGCTGGATGCTTCAGTCGTGTGGAGAC 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 GGACCGGAGACGCTCTGCCGGCTGAGCTGGATGCTTCAGTCGTGTGGAGAC 60

Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 AGGGGCTTTATTCAACAAGCCCACAGGATACTGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy 181 TGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 TGTGCACCCCTCAAGCCGGAAAGGCAGCCGCTCCGTGCCAGCGCCACACCGAC 240

Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 241 ATGCCCAAGACTCAG----- 255

Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 256 -----AAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 311

Qy 361 GATGTA-GAAGACCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC 419
||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 312 GATGTAGGAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC 371

Qy 420 TGCACAGTTACCTGTAAACATTGGAAATACGGCCAAAAATAAGTTGATCACATTCAA 479
||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 372 TGCACAGTTACCTGTAAACATTGGAAATACGGCCAAAAATAAGTTGATCACATTCAA 431

Qy 480 AGATGGCATTCCCCAATGAAATACACAAGTAAACAT 517
||| ||| ||| ||| ||| ||| ||| |||

Db 432 AGATGGCATTCCCCAATGAAATACACAAGTAAACAT 469

RESULT 6

AX300791

LOCUS AX300791 471 bp DNA linear PAT 30-NOV-2001

DEFINITION Sequence 13 from Patent WO0185781.

ACCESSION AX300791

VERSION AX300791.1 GI:17382072

KEYWORDS

SOURCE Oryctolagus cuniculus (rabbit)

ORGANISM Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 AUTHORS Goldspink, G.D. and Terenghi, G.B.
 TITLE Repair of nerve damage
 JOURNAL Patent: WO 0185781-A 13 15-NOV-2001;
 University College London (GB) ; East Grinstead Medical Research
 Trust (GB)
 FEATURES Location/Qualifiers
 source 1. .471
 /organism="Oryctolagus cuniculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:9986"
 CDS <1. .318
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAD13045.1"
 /db_xref="GI:17382073"
 /translation="GPETLCGAELVDALQFVCGRGFYFNKPTGYGSSSRRAPQTGIV
 DECCFRSCDLRREMYCAPLKAARKSVAQRHTDMPKTQKEVHLKNTSRGSAGNKN
 YRM"
 BASE COUNT 132 a 118 c 131 g 90 t
 ORIGIN
 Query Match 73.0%; Score 377.2; DB 6; Length 471;
 Best Local Similarity 87.8%; Pred. No. 5.4e-110;
 Matches 455; Conservative 0; Mismatches 13; Indels 50; Gaps 2;

```

Qy      1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGATGCTCTCAGTTCTGTGTGGAGAC 60
Db      1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGATGCTCTCAGTTCTGTGTGGAGAC 60

Qy      61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
Db      61 AGGGGCTTTATTCAACAAGCCCACAGGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
Db      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGCCAGGCCACACCGAC 240
Db      181 TGTGCACCCCTCAAGCCGGAAAGGCAGGCCGCTCCGTGCCAGGCCACACCGAC 240

Qy      241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
Db      241 ATGCCCAAGACTCAG----- 255

Qy      301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
Db      256 ----AAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 311

Qy      361 GATGTA-GAAGACCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC 419
Db      312 GATGTAGGAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC 371

Qy      420 TGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTCAA 479

```

Db 372 TGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTCAA 431
 Qy 480 AGATGGCATTCCCCAATGAAATACACAAGTAAACAT 517
 |||||||
 Db 432 AGATGGCATTCCCCAATGAAATACACAAGTAAACAT 469

RESULT 7

HSU40870

LOCUS HSU40870 444 bp mRNA linear PRI 05-APR-1996
 DEFINITION Human alternatively spliced human insulin-like growth factor-I
 (IGF-I) mRNA, partial cds.
 ACCESSION U40870
 VERSION U40870.1 GI:1100902
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 444)
 AUTHORS Chew,S.L., Lavender,P., Clark,A.J. and Ross,R.J.
 TITLE An alternatively spliced human insulin-like growth factor-I
 transcript with hepatic tissue expression that diverts away from
 the mitogenic IBE1 peptide
 JOURNAL Endocrinology 136 (5), 1939-1944 (1995)
 MEDLINE 95237119
 PUBMED 7720641
 REFERENCE 2 (bases 1 to 444)
 AUTHORS Chew,S.L.
 TITLE Direct Submission
 JOURNAL Submitted (20-NOV-1995) Shern L. Chew, Endocrinology, St
 Bartholomew's Hospital Medical College, West Smithfield, London,
 EC1A 7Be, UK
 FEATURES Location/Qualifiers
 source 1. .444
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="pC4"
 /tissue_type="liver"
 gene 1. .444
 /gene="IGF-I"
 CDS <1. .420
 /gene="IGF-I"
 /note="alternatively spliced; previously, exon 5 and 6
 were thought to be mutually exclusive; this transcript
 splices from exon 5 into exon 6; the alternatively spliced
 transcript would continue with exon 5 to the polyA signal"
 /codon_start=1
 /product="insulin-like growth factor-I"
 /protein_id="AAA96152.1"
 /db_xref="GI:1100903"
 /translation="LKVKMHTMSSSHLFYLALCLLTFTSSATAGPETLCGAEVDALQ
 FVCGRGFYFNKPTGYGSSRAPQTGIVDECCFRSCDLRRLEMYCAPLPAKSARSV
 RAQRHTDMPKTQKYQPPSTNKNTKSQRRKGSTFEERK"
 exon 1. .6
 /gene="IGF-I"

		/number=1		
exon		7. .163		
		/gene="IGF-I"		
		/number=3		
exon		164. .345		
		/gene="IGF-I"		
		/number=4		
exon		346. .394		
		/gene="IGF-I"		
		/number=5		
exon		395. .420		
		/gene="IGF-I"		
		/number=6		
BASE COUNT	107 a	125 c	125 g	87 t
ORIGIN				

Query Match 68.7%; Score 355.4; DB 9; Length 444;
Best Local Similarity 99.7%; Pred. No. 5.7e-103;
Matches 356; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	GGACCGGAGACGCTCTGCGGGCTGAGCTGGATGCTCTCAGTTCGTGTGGAGAC	60
Db	88	GGACCGGAGACGCTCTGCGGGCTGAGCTGGATGCTCTCAGTTCGTGTGGAGAC	147
Qy	61	AGGGGCTTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	120
Db	148	AGGGGCTTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	207
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	208	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	267
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGGCCAACACCGAC	240
Db	268	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGGCCAACACCGAC	327
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA	300
Db	328	ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA	387
Qy	301	AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	357
Db	388	AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	444

RESULT 8

HSIGF1A

LOCUS HSIGF1A 616 bp mRNA linear PRI 29-NOV-1993

DEFINITION H.sapiens mRNA for IGF-1a.

ACCESSION X56773 S61841

VERSION X56773.1 GI:32989

KEYWORDS IGF-1 gene.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 616)

AUTHORS Sandberg-Nordqvist,A.C., Stahlbom,P.A., Lake,M. and Sara,V.R.
 TITLE Characterization of two cDNAs encoding insulin-like growth factor 1
 (IGF-1) in the human fetal brain
 JOURNAL Brain Res. Mol. Brain Res. 12 (1-3), 275-277 (1992)
 MEDLINE 92186627
 PUBMED 1372070
 REFERENCE 2 (bases 1 to 616)
 AUTHORS Sandberg Nordqvist,A.C.
 TITLE Direct Submission
 JOURNAL Submitted (19-NOV-1990) A.C.Sandberg Nordqvist, KAROLINSKA INST'S
 DEPT OF PATHOLOGY, KAROLINSKA HOSPITAL, BOX 605 00, S-104 01
 STOCKHOLM, SWEDEN
 REFERENCE 3 (bases 1 to 616)
 AUTHORS Sandberg-Nordqvist,A.C., Stahlbom,P.A., Reinecke,M., Collins,V.P.,
 von Holst,H. and Sara,V.
 TITLE Characterization of insulin-like growth factor 1 in human primary
 brain tumors
 JOURNAL Cancer Res. 53 (11), 2475-2478 (1993)
 MEDLINE 93265440
 PUBMED 8495408
 FEATURES Location/Qualifiers
 source 1. .616
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="12"
 /map="q22-q24"
 /tissue_type="brain"
 /dev_stage="fetal"
 gene 1. .462
 /gene="IGF-1"
 CDS 1. .462
 /gene="IGF-1"
 /codon_start=1
 /product="IGF-1a"
 /protein_id="CAA40092.1"
 /db_xref="GI:32990"
 /db_xref="SWISS-PROT:P01343"
 /translation="MGKISSLPTQLFKCCFCDFLKVKMHTMSSSHLFYLALCLLTFTS
 SATAGPETLCGAELVDALQFVCGRGFYFNKPTGYGSSSRAPQTGIVDECCFRSCDL
 RRLEMYCAPLPAKSARSVRAQRHTDMPKTQKEVHLKNASRGSGAGNKNYRM"
 mat_peptide 145. .354
 /gene="IGF-1"
 /product="IGF-1a"
 exon 403. .616
 /note="exon 5"
 BASE COUNT 159 a 158 c 160 g 139 t
 ORIGIN

Query Match 66.6%; Score 344.2; DB 9; Length 616;
 Best Local Similarity 87.3%; Pred. No. 2.5e-99;
 Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy. 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGATGCTTCAGTCGTGTGGAGAC 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 145 GGACCGGAGACGCTCTGCGGGCTGAGCTGGATGCTTCAGTCGTGTGGAGAC 204

Qy	61	AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	120
Db	205	AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	264
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	265	ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	324
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240
Db	325	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	384
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA	300
		-----	-----
Db	385	ATGCCCAAGACCCAG-----	399
		-----	-----
Qy	301	AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	360
Db	400	---AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	455
	-----	-----	-----
Qy	361	GATGTA-GAACACCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC	419
Db	456	GATGTAGGAAGACCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC	515
Qy	420	TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC	477
Db	516	TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTAA	575
	-----	-----	-----
Qy	478	AAAGAT-GGCATTCCCCAATGAAATACACAAGTAAACAT	517
Db	576	AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT	616

RESULT 9

AX375028

LOCUS	AX375028	7260 bp	DNA	linear	PAT 01-MAR-2002
DEFINITION	Sequence 31 from Patent WO0210436.				
ACCESSION	AX375028				
VERSION	AX375028.1	GI:19169860			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Baak, J. and Mutter, G.L.				
TITLE	Prognostic classification of breast cancer				
JOURNAL	Patent: WO 0210436-A 31 07-FEB-2002; THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; Baak, Jan (US)				
FEATURES	Location/Qualifiers				
source	1. .7260 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"				
BASE COUNT	2330	a	1415	c	1240 g 2275 t
ORIGIN					

Query Match 66.6%; Score 344.2; DB 6; Length 7260;
 Best Local Similarity 87.3%; Pred. No. 3.6e-99;
 Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy	1	GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTTCAGTTCTGTGTGGAGAC	60
Db	311	GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTTCAGTTCTGTGTGGAGAC	370
Qy	61	AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG	120
Db	371	AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG	430
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	431	ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	490
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240
Db	491	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	550
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA	300
		-----	-----
Db	551	ATGCCCAAGACCCAG-----	565
Qy	301	AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	360
Db	566	---AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	621
Qy	361	GATGTA-GAAGACCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTGCTC	419
Db	622	GATGTAGGAAGACCCCTCGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC	681
Qy	420	TGCAC-AGTTACCTG-TAAACATTGAAATACCGGCCAAAAATAAGTTGATCACATTTC	477
Db	682	TGCACGAGTTACCTGTTAAACTTGAACACCTACCAAAAAATAAGTTGATAACATTTC	741
Qy	478	AAAGAT-GGCATTCCCCAATGAAATACACAAGTAAACAT	517
Db	742	AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT	782

RESULT 10

AX411095

LOCUS AX411095 7260 bp DNA linear PAT 14-JUN-2002
 DEFINITION Sequence 3742 from Patent WO0229103.
 ACCESSION AX411095
 VERSION AX411095.1 GI:21443800
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G.
 TITLE Gene expression profiles in liver cancer
 JOURNAL Patent: WO 0229103-A 3742 11-APR-2002;
 GENE LOGIC INC (US)

FEATURES Location/Qualifiers
source
 1..7260
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /note="EMBL/GenBank Accession No. X57025"

BASE COUNT 2330 a 1415 c 1240 g 2275 t
ORIGIN

Query Match 66.6%; Score 344.2; DB 6; Length 7260;
 Best Local Similarity 87.3%; Pred. No. 3.6e-99;
 Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy	1 GGACCGGAGACGCTCTGGGGCTGAGCTGGTGGATGCTTCAGTTCGTGTGGAGAC	60
Db	311 GGACCGGAGACGCTCTGGGGCTGAGCTGGTGGATGCTTCAGTTCGTGTGGAGAC	370
Qy	61 AGGGGCTTTATTCACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG	120
Db	371 AGGGGCTTTATTCACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG	430
Qy	121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	431 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	490
Qy	181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240
Db	491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	550
Qy	241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA	300
Db	551 ATGCCCAAGACCCAG-----	565

Qy	301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	360
Db	566 ---AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	621

Qy	361 GATGTA-GAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTGCTC	419
Db	622 GATGTAGGAAGACCCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC	681
Qy	420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC	477
Db	682 TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTAA	741
Qy	478 AAAGAT-GGCATTCCCCAATGAAATACACAAGTAAACAT	517
Db	742 AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT	782

RESULT 11
HSIGFACI
LOCUS HSIGFACI 7260 bp mRNA linear PRI 17-FEB-1992
DEFINITION Human IGF-I mRNA for insulin-like growth factor I.
ACCESSION X57025
VERSION X57025.1 GI:33007
KEYWORDS insulin-like growth factor I.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 7260)
 AUTHORS Steenbergh, P.H., Koonen-Reemst, A.M., Cleutjens, C.B. and
 Sussenbach, J.S.
 TITLE Complete nucleotide sequence of the high molecular weight human
 IGF-I mRNA
 JOURNAL Biochem. Biophys. Res. Commun. 175 (2), 507-514 (1991)
 MEDLINE 91207342
 PUBMED 2018498
 REFERENCE 2 (bases 1 to 7260)
 AUTHORS Steenbergh, P.H.
 TITLE Direct Submission
 JOURNAL Submitted (18-DEC-1990) P.H. Steenbergh, LAB FOR PHYSIOLOGICAL
 CHEMISTRY, UNIVERSITY OF UTRECHT, VONDELLAAN 24 A, 3521 GG UTRECHT,
 THE NETHERLANDS
 FEATURES Location/Qualifiers
 source 1. .7260
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="12 q22-24.1"
 /tissue_type="liver"
 /dev_stage="adult"
 gene 1. .7260
 /gene="IGF-I"
 mRNA 1. .7260
 /gene="IGF-I"
 /evidence=experimental
 exon 1. .229
 /gene="IGF-I"
 /number=1
 /evidence=experimental
 CDS 167. .628
 /gene="IGF-I"
 /codon_start=1
 /evidence=experimental
 /product="insulin-like growth factor I"
 /protein_id="CAA40342.1"
 /db_xref="GI:33008"
 /db_xref="SWISS-PROT:P01343"
 /translation="MGKISSLPTQLFKCCFCDFLKVKMHTMSSSHLFYLALCLLTFTS
 SATAGPETLCGAEVLDALQFVCGDRGFYFNKPTGYGSSSRAPQTGIVDECCFRSCDL
 RRLEMYCAPLPAKSARSVRAQRHTDMPKTQKEVHLKNASRGSGAGNKNYRM"
 sig_peptide 167. .310
 /gene="IGF-I"
 /evidence=experimental
 mat_peptide 311. .520
 /gene="IGF-I"
 /product="insulin-like growth factor I"
 /evidence=experimental
 exon 230. .386
 /gene="IGF-I"
 /number=2
 /evidence=experimental

BASE COUNT 2330 a 1415 c 1240 g 2275 t
ORIGIN

Db 622 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC 681
 Qy 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC 477
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 682 TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAAACATTTA 741
 Qy 478 AAAGAT-GGCATTTCCCCAATGAAATACACAAGTAAACAT 517
 ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 742 AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT 782

RESULT 12

A29119

LOCUS A29119 666 bp DNA linear PAT 15-JUN-1995
 DEFINITION H.sapiens IGF1 gene fragment from patent GB2241703.
 ACCESSION A29119
 VERSION A29119.1 GI:1247520
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 666)
 AUTHORS
 JOURNAL Patent: GB 2241703-A 3 11-SEP-1991;
 FEATURES Location/Qualifiers
 source 1. .666
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 CDS 25. .384
 /partial
 /codon_start=1
 /product="IGF-1 precursor"
 /protein_id="CAA01955.1"
 /db_xref="GI:4529932"
 /translation="MALCLLTFTSSATAGPETLCGAELVDALQFVCGDRGFYFNKPTG
 YGSSSRRAPQTGIVDECCFRSCDLRRLEMYCAPLPAKSARSVRQRHTDMPKTQKEV
 HLKNASRGSGAGNKNYRM"
 mat_peptide 67. .276
 /product="IGF-1"
 BASE COUNT 173 a 167 c 181 g 145 t
 ORIGIN

Query Match 66.3%; Score 342.6; DB 6; Length 666;
 Best Local Similarity 87.1%; Pred. No. 8.2e-99;
 Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;
 Qy 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGATGCTTCAGTCGTGTGGAGAC 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 67 GGACCGGAGACGCTCTGCGGGCTGAGCTGGATGCTTCAGTCGTGTGGAGAC 126
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 61 AGGGCTTTATTCACAAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCCCTCAG 120
 ||||| ||||| ||||| ||||| ||||| |||||
 Db 127 AGGGCTTTATTCACAAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCCCTCAG 186
 Qy 121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Db	187	ACAGGTATCGTGGATGAGTGCTGCTTCGGAGCTGTATCTAAGGAGGCTGGAGATGTAT	246
Qy	181	TGCGCACCCCTCAAGCCTGCCAACGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240
Db	247	TGCGCACCCCTCAAGCCTGCCAACGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	306
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA	300
Db	307	ATGCCCAAGACCCAG-----	321
Qy	301	AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	360
Db	322	---AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	377
Qy	361	GATGTA-GAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC	419
Db	378	GATGTAGGAAGACCCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC	437
Qy	420	TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCAAAAAATAAGTTGATCACATTTC	477
Db	438	TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTAA	497
Qy	478	AAAGAT-GGCATTCCCCCAATGAAATACACAAGTAAACAT	517
Db	498	AAAGATGGCGTTCCCCCAATGAAATACACAAGTAAACAT	538

RESULT 13

HSIGFI

LOCUS HSIGFI 725 bp mRNA linear PRI 11-DEC-1998
 DEFINITION Homo sapiens mRNA for insulin-like growth factor 1A precursor, complete CDS.
 ACCESSION X00173
 VERSION X00173.1 GI:33015
 KEYWORDS growth factor; insulin super family; insulin-like growth factor I; signal peptide; somatomedin.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Jansen,M., van Schaik,F.M., Ricker,A.T., Bullock,B., Woods,D.E., Gabbay,K.H., Nussbaum,A.L., Sussenbach,J.S. and Van den Brande,J.L.
 TITLE Sequence of cDNA encoding human insulin-like growth factor I precursor
 JOURNAL Nature 306 (5943), 609-611 (1983)
 MEDLINE 84068210
 PUBMED 6358902
 COMMENT Data kindly reviewed (28-MAY-1984) by M. Jansen.
 FEATURES Location/Qualifiers
 source 1..725
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 gene 1..725
 /gene="IGF-1"

CDS 12. .473
 /gene="IGF-1"
 /codon_start=1
 /product="insulin-like growth factor 1A precursor"
 /protein_id="CAA24998.1"
 /db_xref="GI:33016"
 /db_xref="SWISS-PROT:P01343"
 /translation="MGKISSLPTQLFKCCFCDFLKVKMHTMSSHLFYLALCLLTFTS
 SATAGPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRAPQTGIVDECCFRSCDL
 RRLEMYCPLKPAKSARSVRAQRHTDMPKTQEVHLKNASRGSAGNKNYRM"

polyA_site 725
 /gene="IGF-1"

BASE COUNT 190 a 174 c 183 g 178 t
 ORIGIN

Query Match 66.3%; Score 342.6; DB 9; Length 725;
 Best Local Similarity 87.1%; Pred. No. 8.3e-99;
 Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;

Qy	1	GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC	60
Db	156	GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC	215
Qy	61	AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG	120
Db	216	AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG	275
Qy	121	ACAGGCATCGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	276	ACAGGTATCGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	335
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGTCGCTCTGTCCGTGCCAGGCCAACCGAC	240
Db	336	TGCGCACCCCTCAAGCCTGCCAAGTCAGTCGCTCTGTCCGTGCCAGGCCAACCGAC	395
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA	300
		-----	-----
Db	396	ATGCCCAAGACCCAG-----	410
	-----	-----	-----
Qy	301	AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	360
Db	411	---AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	466
	-----	-----	-----
Qy	361	GATGTA-GAACACCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC	419
Db	467	GATGTAGGAAGACCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC	526
Qy	420	TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC	477
Db	527	TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTAA	586
	-----	-----	-----
Qy	478	AAAGAT-GGCATTCCCCAATGAAATACACAAGTAAACAT	517
Db	587	AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT	627

HUMGFI
 LOCUS HUMGFI 728 bp mRNA linear PRI 08-NOV-1994
 DEFINITION Human insulin-like growth factor I mRNA, complete cds.
 ACCESSION M29644
 VERSION M29644.1 GI:183119
 KEYWORDS insulin-like growth factor.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 728)
 AUTHORS Rall,L.B., Scott,J. and Bell,G.I.
 TITLE Human insulin-like growth factor I and II messenger RNA: isolation
 of complementary DNA and analysis of expression
 JOURNAL Meth. Enzymol. 146, 239-248 (1987)
 MEDLINE 88065102
 PUBMED 3683205
 COMMENT Original source text: Human (adult) liver, cDNA to mRNA.
 FEATURES
 source Location/Qualifiers
 1. .728
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /map="12q23"
 gene 1. .728
 /gene="IGF1"
 CDS 81. .473
 /gene="IGF1"
 /note="insulin-like growth factor I precursor"
 /codon_start=1
 /protein_id="AAA52543.1"
 /db_xref="GI:183120"
 /db_xref="GDB:G00-120-081"
 /translation="MHTMSSSHLFYLALCLLFTSSATAGPETLCGAELVDALQFVCG
 DRGFYFNKPTGYGSSSSRAPQTGIVDECCFRSCDLRRLEMYCAPLPAKSARSVRQR
 HTDMPKTQKEVHLKNASRGSAGNKNYRM"
 sig_peptide 81. .155
 /gene="IGF1"
 mat_peptide 156. .365
 /gene="IGF1"
 /product="insulin-like growth factor I"
 BASE COUNT 193 a 174 c 183 g 178 t
 ORIGIN Chromosome 12q23.

Query Match 66.3%; Score 342.6; DB 9; Length 728;
 Best Local Similarity 87.1%; Pred. No. 8.3e-99;
 Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;

Qy	1	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC	60
Db	156	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC	215
Qy	61	AGGGGTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG	120
Db	216	AGGGGTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG	275

QY 121 ACAGGCATCGTGGATGAGTGCTGCTTCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
 ||||| |||||
 Db 276 ACAGGTATCGTGGATGAGTGCTGCTTCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 335
 |||||
 QY 181 TCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGGCCAACCGAC 240
 |||||
 Db 336 TCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGGCCAACCGAC 395
 |||||
 QY 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
 |||||
 Db 396 ATGCCCAAGACCCAG----- 410
 |||||
 QY 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
 |||||
 Db 411 ---AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 466
 |||||
 QY 361 GATGTA-GAAGACCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC 419
 |||||
 Db 467 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC 526
 |||||
 QY 420 TGCAC-AGTTACCTG-TAAACATTGAATACCGGCCAAAAATAAGTTGATCACATTTC 477
 |||||
 Db 527 TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTAA 586
 |||||
 QY 478 AAAGAT-GGCATTCCCCAATGAAATACACAAGTAAACAT 517
 |||||
 Db 587 AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT 627

RESULT 15

HUMIGFI

LOCUS HUMIGFI 1076 bp mRNA linear PRI 08-NOV-1994
 DEFINITION Human insulin-like growth factor mRNA, complete cds.
 ACCESSION M27544
 VERSION M27544.1 GI:184829
 KEYWORDS insulin-like growth factor.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1076)
 REFERENCE Le Bouc, Y., Dreyer, D., Jaeger, F., Binoux, M. and Sondermeyer, P.
 TITLE Complete characterization of the human IGF-I nucleotide sequence
 isolated from a newly constructed adult liver cDNA library
 JOURNAL FEBS Lett. 196 (1), 108-112 (1986)
 MEDLINE 86108910
 PUBMED 2935423
 COMMENT Original source text: Human liver, cDNA to mRNA, clones
 lanbda-TG[03,04,05].
 FEATURES Location/Qualifiers
 source 1. .1076
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /map="7p13-p12"
 gene 1. .1076
 /gene="IGFBP1"

mRNA <1. .>1076
 /gene="IGFBP1"
 /note="IGF mRNA (alt.)"
 mRNA <1. .989
 /gene="IGFBP1"
 /note="IGF mRNA (alt.)"
 CDS 149. .610
 /gene="IGFBP1"
 /note="insulin-like growth factor precursor"
 /codon_start=1
 /protein_id="AAA52787.1"
 /db_xref="GI:306927"
 /db_xref="GDB:G00-120-075"
 /translation="MGKISSLPTQLFKCCFCDFLKVKMHTMSSSHLFYLALCLLTFTS
 SATAGPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRAPQTGIVDECCFRSCDL
 RRLEMYCPLKPAKSARSVRQRHTDMPKTQKEVHLKNASRGSAGNKNYRM"
 sig_peptide 149. .292
 /gene="IGFBP1"
 /note="insulin-like growth factor signal peptide"
 mat_peptide 293. .502
 /gene="IGFBP1"
 /product="insulin-like growth factor"
 BASE COUNT 283 a 251 c 239 g 303 t
 ORIGIN Chromosome 7p13-p12.

Query Match 66.3%; Score 342.6; DB 9; Length 1076;
 Best Local Similarity 87.1%; Pred. No. 8.8e-99;
 Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;

Qy	1	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGATGCTTCAGTTCTGTGTGGAGAC	60
Db	293	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGATGCTTCAGTTCTGTGTGGAGAC	352
Qy	61	AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG	120
Db	353	AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG	412
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	413	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	472
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240
Db	473	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	532
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA	300

Db	533	ATGCCCAAGACCCAG-----	547

Qy	301	AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	360
Db	548	---AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	603

Qy	361	GATGTA-GAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC	419
Db	604	GATGTAGGAAGACCCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC	663

Qy 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC 477
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 664 TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTAA 723
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 478 AAAGAT-GGCATTTCCCCAATGAAATACACAAGTAAACAT 517
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 724 AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACTT 764

Search completed: December 13, 2003, 09:27:32
Job time : 2313.97 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 02:35:18 ; Search time 207.586 Seconds
(without alignments)
6723.048 Million cell updates/sec

Title: US-09-852-261-1

Perfect score: 517

Sequence: 1 ggaccggagacgctctgcgg.....tgaaatacacaagtaaacat 517

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*

8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*

10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*

11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*

12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*

13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*

14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*

15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*

16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*

17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*

18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*

19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*

20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*

22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*

24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	517	100.0	517	22	AAD06398	Human IGF-I isoform
2	517	100.0	517	24	AAS16877	Human mechano-grow
3	467.4	90.4	523	22	AAD06400	Rabbit IGF-I isoform
4	467.4	90.4	523	24	AAS16879	Rabbit mechano-grow
5	467.4	90.4	553	18	AAT84893	Rabbit insulin like
6	377.2	73.0	471	22	AAD06405	Rabbit liver-type
7	377.2	73.0	471	24	AAS16884	Rabbit insulin-like
8	344.2	66.6	818	8	AAN70436	Sequence encoding
9	344.2	66.6	7260	24	ABT11091	Human breast cancer
10	344.2	66.6	7260	24	ABK84583	Human cDNA difference
11	344.2	66.6	7260	24	ABN97244	Gene #3742 used to
12	344.2	66.6	7260	24	ABK64812	Human benign prostate
13	344.2	66.6	7260	24	ABK35504	Human endometrial
14	344.2	66.6	7260	24	ABK35561	Gene IGF1 difference
15	342.6	66.3	777	18	AAT84894	Human insulin like
16	339.4	65.6	622	7	AAN60490	Human prepro-somatotropin
17	325.2	62.9	539	22	AAD06399	Rat IGF-I isoform
18	325.2	62.9	539	24	AAS16878	Rat mechano-growth
19	318.2	61.5	651	25	ABV76185	Mouse insulin-like
20	308.6	59.7	1136	8	AAN70435	Sequence encoding
21	286.4	55.4	3599	19	AAV50428	Plasmid pIG0552 lower
22	286.4	55.4	3599	19	AAV40796	Actual sequence of
23	286.4	55.4	3600	19	AAV50427	Plasmid pIG0552 upper
24	286.4	55.4	3600	19	AAV40795	Expected sequence
25	286.4	55.4	5707	20	AAX88055	Plasmid pIG0335 DNA
26	286.4	55.4	6345	20	AAX88054	Plasmid pIG0100A DNA
27	285.4	55.2	612	22	AAS14695	Human cDNA encoding
28	285.4	55.2	612	25	ABZ83309	Toxicologically relevant
29	271.2	52.5	978	14	AAQ47804	Sequence encoding
30	258.4	50.0	317	24	AAS16882	Human insulin-like
31	258.4	50.0	318	22	AAD06403	Human liver-type I
32	258.4	50.0	462	19	AAV50426	Human IGF-1 encoding
33	258.4	50.0	462	19	AAV40794	Human IGF-I coding
34	258.4	50.0	462	24	ABZ35734	Human IGF1 polynucleotide
35	258.4	50.0	462	24	ABX09977	Human IGF1 DNA fragment
36	258.4	50.0	462	24	ABV78158	Human IGF1 DNA SEQ
37	258.4	50.0	462	24	ABL91699	Human polynucleotide
38	252.6	48.9	1052	20	AAX27498	Rat liver form of
39	247.8	47.9	487	22	AAD06404	Rat liver-type IGF
40	247.8	47.9	487	24	AAS16883	Rat insulin-like gene
41	234.2	45.3	671	24	ABT09479	Phase-1 Rat CT gene
42	210	40.6	210	24	AAD45568	Human insulin-like
43	210	40.6	210	24	AAD44955	Human insulin growth
44	210	40.6	210	24	ABA03146	Native mature IGF-
45	208.4	40.3	237	12	AAQ13568	Beta-gal/IGF-1 fusion

ALIGNMENTS

RESULT 1
AAD06398

ID AAD06398 standard; cDNA; 517 BP.
XX
AC AAD06398;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human IGF-I isoform mechano-growth factor (MGF) cDNA.
XX
KW Human; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW sex-linked muscular dystrophy; peripheral neuropathy;
KW Alzheimer's disease; Parkinson's disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..333
FT /*tag= a
FT /product= "Mechano-growth factor (MGF)"
FT /note= "This region comprises exons 3-6. The CDS does
FT not include start codon"
FT /partial
XX
PN WO200136483-A1.
XX
PD 25-MAY-2001.
XX
PF 15-NOV-2000; 2000WO-GB04354.
XX
PR 15-NOV-1999; 99GB-0026968.
XX
PA (UNLO) UNIV COLLEGE LONDON.
XX
PI Goldspink G, Johnson I;
XX
DR WPI; 2001-355620/37.
DR P-PSDB; AAE02447.
XX
PT Use of mechano-growth factor, an isoform of Insulin-like Growth
PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PT medicament for the treatment of neurological disorder -
XX
PS Claim 4; Page 49-50; 66pp; English.
XX
CC The present invention relates to use of mechano-growth factor (MGF),
CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC medicament for the treatment of neurological disorder. The MGF is capable
CC of reducing motoneurone loss by 20% or greater in response to nerve
CC avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC rescue. The MGF polynucleotide and polypeptide are useful in the
CC manufacture of a medicament for the treatment of a neurological disorder,

CC including a disorder of motoneurones and/or neurodegenerative disorder,
CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC injury that affects motoneurones, motoneurone loss associated with aging,
CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC The present sequence is human IGF-I isoform MGF cDNA. MGF is a muscle
CC isoform having extracellular (Ec) domain, hence also referred as
CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
CC of MGF.

XX

SQ Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

Query Match 100.0%; Score 517; DB 22; Length 517;
Best Local Similarity 100.0%; Pred. No. 1.6e-146;
Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGATGCTCTTCAGTTCTGTGTGGAGAC 60
Db 1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGATGCTCTTCAGTTCTGTGTGGAGAC 60

Qy 61 AGGGGCTTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 120
Db 61 AGGGGCTTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 120

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
Db 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy 181 TGCGCACCCCTCAAGCCTGCCAACGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
Db 181 TGCGCACCCCTCAAGCCTGCCAACGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240

Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
Db 241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300

Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
Db 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360

Qy 361 GATGTAGAACGCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTGCTCT 420
Db 361 GATGTAGAACGCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTGCTCT 420

Qy 421 GCACAGTTACCTGTAAACATTGAAATCCGGCAAAAAATAAGTTGATCACATTCAA 480
Db 421 GCACAGTTACCTGTAAACATTGAAATCCGGCAAAAAATAAGTTGATCACATTCAA 480

Qy 481 GATGGCATTCCCCAATGAAATACACAAGTAAACAT 517
Db 481 GATGGCATTCCCCAATGAAATACACAAGTAAACAT 517

RESULT 2

AAS16877

ID AAS16877 standard; cDNA; 517 BP.

XX

AC AAS16877;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human mechano-growth factor (MGF) cDNA.

XX

KW Human; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;
KW nerve avulsion.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..333

FT /*tag= a

FT /product= "Human MGF"

FT /partial

FT /note= "No start codon"

FT exon 1..76

FT /*tag= b

FT /number= 3

FT exon 77..259

FT /*tag= c

FT /number= 4

FT exon 260..307

FT /*tag= d

FT /number= 5

FT exon 308..330

FT /*tag= e

FT /number= 6

XX

PN WO200185781-A2.

XX

PD 15-NOV-2001.

XX

PF 10-MAY-2001; 2001WO-GB02054.

XX

PR 10-MAY-2000; 2000GB-0011278.

XX

PA (UNLO) UNIV COLLEGE LONDON.

PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.

XX

PI Goldspink G, Terenghi G;

XX

DR WPI; 2002-055585/07.

DR P-PSDB; AAU10559.

XX

PT Use of insulin-like growth factor I (IGF-I) isoform known as
PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT ability to reduce motoneuron loss in response to nerve avulsion, to
PT treat nerve damage -

XX

PS Claim 11; Fig 5; 65pp; English.

XX

CC The invention relates to the use of an insulin-like growth factor I
CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC of a medicament for treating nerve damage in the peripheral nervous
CC system, or for treating nerve damage by localising MGF at the site of
CC damage. The nerve damage may include severing of a nerve. The treatment
CC may be combined with another treatment (such as a polypeptide growth
CC factor other than MGF) that prevents or diminishes degeneration of the
CC target organ (for example, muscle) which the damaged nerve innervates,
CC whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC MGF prevents or diminishes degeneration. The method is useful for
CC treating neurological disorders, preferably motoneuron disorders. These
CC methods can reduce motoneuron loss by 20% or greater in response to nerve
CC avulsion. This sequence represents cDNA encoding the human MGF.

XX

SQ Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

Query Match 100.0%; Score 517; DB 24; Length 517;
Best Local Similarity 100.0%; Pred. No. 1.6e-146;
Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGATGCTTCAGTCGTGTGGAGAC 60
Db 1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGATGCTTCAGTCGTGTGGAGAC 60

Qy 61 AGGGGCTTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCCCTCAG 120
Db 61 AGGGGCTTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCCCTCAG 120

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
Db 121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCACACCGAC 240
Db 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCACACCGAC 240

Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
Db 241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300

Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
Db 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360

Qy 361 GATGTAGAACGCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTGCTCT 420
Db 361 GATGTAGAACGCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTGCTCT 420

Qy 421 GCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTCAA 480
Db 421 GCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTCAA 480

Qy 481 GATGGCATTTCCCCAATGAAATACACAAGTAAACAT 517
Db 481 GATGGCATTTCCCCAATGAAATACACAAGTAAACAT 517

RESULT 3
AAD06400
ID AAD06400 standard; cDNA; 523 BP.
XX
AC AAD06400;
XX
DT 10-AUG-2001 (first entry)
XX
DE Rabbit IGF-I isoform mechano-growth factor (MGF) cDNA.
XX
KW Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW sex-linked muscular dystrophy; peripheral neuropathy;
KW Alzheimer's disease; Parkinson's disease; ss.
XX
OS Oryctolagus cuniculus.
XX
FH Key Location/Qualifiers
FT CDS 1..336
FT /*tag= a
FT /product= "Mechano-growth factor (MGF)"
FT /note= "This region comprises exons 3-6. The CDS does
FT not include start codon"
FT /partial
XX
PN WO200136483-A1.
XX
PD 25-MAY-2001.
XX
PF 15-NOV-2000; 2000WO-GB04354.
XX
PR 15-NOV-1999; 99GB-0026968.
XX
PA (UNLO) UNIV COLLEGE LONDON.
XX
PI Goldspink G, Johnson I;
XX
DR WPI; 2001-355620/37.
DR P-PSDB; AAE02449.
XX
PT Use of mechano-growth factor, an isoform of Insulin-like Growth
PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PT medicament for the treatment of neurological disorder -
XX
PS Claim 4; Page 53-54; 66pp; English.
XX
CC The present invention relates to use of mechano-growth factor (MGF),
CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC medicament for the treatment of neurological disorder. The MGF is capable
CC of reducing motoneurone loss by 20% or greater in response to nerve
CC avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC rescue. The MGF polynucleotide and polypeptide are useful in the

CC manufacture of a medicament for the treatment of a neurological disorder,
CC including a disorder of motoneurones and/or neurodegenerative disorder,
CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC injury that affects motoneurones, motoneurone loss associated with aging,
CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC The present sequence is rabbit IGF-I isoform MGF cDNA. MGF is a muscle
CC isoform having extracellular (Ec) domain, hence also referred as
CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
CC of MGF.

XX

SQ Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Query Match 90.4%; Score 467.4; DB 22; Length 523;
Best Local Similarity 96.2%; Pred. No. 1.8e-131;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTTCAGTTCTGTGTGGAGAC 60
Db 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTTCAGTTCTGTGTGGAGAC 60

Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 120
Db 61 AGGGGCTTTATTCAACAAGCCCACAGGATAACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
Db 121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy 181 TGCGACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
Db 181 TGTGCACCCCTCAAGCCGAAAGGCAGCCGCTCCGTGCCAGCGCCACACCGAC 240

Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
Db 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy 298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
Db 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy 358 CAGGATGTA-GAAGACCCCTCTGAGGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTG 416
Db 361 CAGGATGTAGGAAGACCCCTCTGAGGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTG 420

Qy 417 CTCTGCACAGTTACCTGTAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTT 476
Db 421 CTCTGCACAGTTACCTGTAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTT 480

Qy 477 CAAAGATGGCATTTCCCCAATGAAATAACACAAGTAAACAT 517
Db 481 CAAAGATGGCATTTCCCCAATGAAATAACACAAGTAAACAT 521

RESULT 4

AAS16879

ID AAS16879 standard; cDNA; 523 BP.

XX

AC AAS16879;

XX

DT 25-FEB-2002 (first entry)

XX

DE Rabbit mechano-growth factor (MGF) cDNA.

XX

KW Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF; neuroprotective; nerve damage; peripheral nervous system; nerve severing; muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss; nerve avulsion.

XX

OS Oryctolagus cuniculus.

XX

FH Key Location/Qualifiers

FT CDS 1..336

FT /*tag= a

FT /product= "Rabbit MGF"

FT /partial

FT /note= "No start codon"

FT exon 1..76

FT /*tag= b

FT /number= 3

FT exon 77..259

FT /*tag= c

FT /number= 4

FT exon 260..309

FT /*tag= d

FT /number= 5

FT exon 311..333

FT /*tag= e

FT /number= 6

XX

PN WO200185781-A2.

XX

PD 15-NOV-2001.

XX

PF 10-MAY-2001; 2001WO-GB02054.

XX

PR 10-MAY-2000; 2000GB-0011278.

XX

PA (UNLO) UNIV COLLEGE LONDON.

PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.

XX

PI Goldspink G, Terenghi G;

XX

DR WPI; 2002-055585/07.

DR P-PSDB; AAU10561.

XX

PT Use of insulin-like growth factor I (IGF-I) isoform known as

PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has

PT ability to reduce motoneuron loss in response to nerve avulsion, to

PT treat nerve damage -

xx

PS Disclosure; Fig 7; 65pp; English.

xx

The invention relates to the use of an insulin-like growth factor I (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture of a medicament for treating nerve damage in the peripheral nervous system, or for treating nerve damage by localising MGF at the site of damage. The nerve damage may include severing of a nerve. The treatment may be combined with another treatment (such as a polypeptide growth factor other than MGF) that prevents or diminishes degeneration of the target organ (for example, muscle) which the damaged nerve innervates, whereby the treatment of the muscle with MGF or a polynucleotide encoding MGF prevents or diminishes degeneration. The method is useful for treating neurological disorders, preferably motoneuron disorders. These methods can reduce motoneuron loss by 20% or greater in response to nerve avulsion. This sequence represents cDNA encoding the rabbit MGF.

xx

SQ Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Query Match 90.4%; Score 467.4; DB 24; Length 523;
Best Local Similarity 96.2%; Pred. No. 1.8e-131;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTCTTCAGTCGTGTGGAGAC 60

Db 1 GGACCCGAGACGCTCTGCCGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

QY 61 AGGGGCTTTTATTTCAACAAAGCCCAAGGGTATGGCTTCAGCAGTCGGAGGGCGGCAG 120

...TTTATTAATGAACTTCAACCTCCAGGGCACCTCAG 120

Qy 121 ACAGGCATCGGGATGAGTGTGCTTCGGAGCTGTATCTAAGGAGGCTGGAGATGTAT 180

Db 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTATCTGAGGGAGGCTGGAGATGTAC 180

Digitized by srujanika@gmail.com

Db 181 TGTGCA~~CC~~CTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCAGCGC~~CA~~ACCGGAC 240

QY 241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAAACAAGAACACGAAGTCTCA---G 297

Figure 1. The effect of the number of hidden neurons on the performance of the proposed model.

QY 298 AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAAACAAGAACTA 357

DB 301 AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

358 CAGGATCTTA GAGGAGCCCTTCTGTGAGATGAGA GAGGAGTGAGA

Ph. 361. SUGGITTICULUS

DB 361 CAGGAATGAGGAAGACCCCTTCTGAGGAGTGAAGAAGGA CAGGCCACCGCAGGACCCTTG 420

QY 417 CTCTGCACAGTTACCTGTAAAATTTGGAAATACCGGCCAAAAAATAAGTTGATCACATT 476

Pb 431 CTCTGCA GACGTT CCTCTT GATTCGAT TCCGGTCTT

Ov 473 CAAGACATGGGATTTCGGGAGTGAAATGCGCTTCAAGTGTGCTT

Db

481 CAAAGATGGCATTCCCCAATGAAATACACAAGTAAACAT 521

RESULT 5

AAT84893

ID AAT84893 standard; cDNA; 553 BP.

XX

AC AAT84893;

XX

DT 14-APR-1998 (first entry)

XX

DE Rabbit insulin like growth factor 1 encoding cDNA.

XX

KW Insulin like growth factor 1; IGF-1; Ec peptide; muscle disorder;

KW heart; neuromuscular disease; primer; ss.

XX

OS Oryctolagus cuniculus.

XX

FH Key Location/Qualifiers

FT CDS 1..366

FT /*tag= a

FT /product= "IGF-1"

XX

PN WO9733997-A1.

XX

PD 18-SEP-1997.

XX

PF 11-MAR-1997; 97WO-GB00658.

XX

PR 11-MAR-1996; 96GB-0005124.

XX

PA (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.

XX

PI Goldspink G;

XX

DR WPI; 1997-470877/43.

DR P-PSDB; AAW23301.

XX

PT Use of insulin like growth factor I characterised by presence of Ec
PT peptide - to treat humans or animals, particularly muscle disorders,
PT heart conditions or neuromuscular diseases

XX

PS Disclosure; Fig 3; 33pp; English.

XX

CC A use of insulin like growth factor I (IGF-1) has been developed, and
CC is characterised by the presence of the Ec peptide, or a functional
CC equivalent, in the treatment or therapy of a human or animal. The IGF-1
CC polypeptide can be used to treat muscular disorders, e.g. Duchenne or
CC Becker muscular dystrophy, autosomal dystrophies and related progressive
CC skeletal muscle weakness and wasting, muscle atrophy in ageing humans,
CC spinal cord injury induced muscle atrophy and neuromuscular diseases,
CC and cardiac disorders, e.g. diseases where promotion of cardiac muscle
CC protein synthesis is a beneficial treatment, cardiomyopathies and acute
CC heart failure or insult, specifically myocarditis or myocardial
CC infarction. It can also be used to promote bone fracture healing and
CC maintenance of bone in old age. The present sequence encodes rabbit
CC IGF-1 used in the present specification.

XX

SQ Sequence 553 BP; 159 A; 142 C; 147 G; 105 T; 0 other;

Query Match 90.4%; Score 467.4; DB 18; Length 553;
Best Local Similarity 96.2%; Pred. No. 1.8e-131;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTCTTCAGTTCTGTGTGGAGAC 60
Db 31 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCTGTGTGGAGAC 90

Qy 61 AGGGGCTTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
Db 91 AGGGGCTTTTATTCAACAAGCCCACAGGATAACGGCTCCAGCAGTCGGAGGGCACCTCAG 150

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
Db 151 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210

Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
Db 211 TGTGCACCCCTCAAGCCGAAAGGCAGCCGCTCCGTGCCAGCGCCACACCGAC 270

Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
Db 271 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 330

Qy 298 AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
Db 331 AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390

Qy 358 CAGGATGTA-GAAGACCCCTCTGAGGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 416
Db 391 CAGGATGTAGGAAGACCCCTCTGAGGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 450

Qy 417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTT 476
Db 451 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTT 510

Qy 477 CAAAGATGGCATTCCCCAATGAAATACACAAGTAAACAT 517
Db 511 CAAAGATGGCATTCCCCAATGAAATACACAAGTAAACAT 551

RESULT 6

AAD06405

ID AAD06405 standard; cDNA; 471 BP.

XX

AC AAD06405;

XX

DT 10-AUG-2001 (first entry)

XX

DE Rabbit liver-type IGF-I isoform (L.IGF-I) cDNA.

XX

KW Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;

KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW sex-linked muscular dystrophy; peripheral neuropathy;
KW Alzheimer's disease; Parkinson's disease; liver; L.IGF-I; ss.
XX
OS Oryctolagus cuniculus.
XX
FH Key Location/Qualifiers
FT CDS 1..318
FT /*tag= a
FT /product= "Liver-type IGF-I isoform (L.IGF-I)"
FT /transl_except= (pos:7..9, aa:Gln)
FT /transl_except= (pos:25..27, aa:Gln)
FT /note= "These translation exceptions occur while decoding
FT the alternative version of the protein (AAE02456).
FT The CDS comprises exons 3, 4 and 6 and
FT does not include start codon"
FT /partial
XX
PN WO200136483-A1.
XX
PD 25-MAY-2001.
XX
PF 15-NOV-2000; 2000WO-GB04354.
XX
PR 15-NOV-1999; 99GB-0026968.
XX
PA (UNLO) UNIV COLLEGE LONDON.
XX
PI Goldspink G, Johnson I;
XX
DR WPI; 2001-355620/37.
DR P-PSDB; AAE02452, AAE02456.
XX
PT Use of mechano-growth factor, an isoform of Insulin-like Growth
PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PT medicament for the treatment of neurological disorder -
XX
PS Disclosure; Page 59-60; 66pp; English.
XX
CC The present invention relates to use of mechano-growth factor (MGF),
CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC medicament for the treatment of neurological disorder. The MGF is capable
CC of reducing motoneurone loss by 20% or greater in response to nerve
CC avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC rescue. The MGF polynucleotide and polypeptide are useful in the
CC manufacture of a medicament for the treatment of a neurological disorder,
CC including a disorder of motoneurones and/or neurodegenerative disorder,
CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC injury that affects motoneurones, motoneurone loss associated with aging,
CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC The present sequence is rabbit liver-type IGF-I isoform (L.IGF-I) cDNA.
CC The L.IGF-I protein comprises amino acid sequences encoded by

CC nucleic acid sequence of IGF-I exons 4 and 6.

XX

SQ Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;

Query Match 73.0%; Score 377.2; DB 22; Length 471;
Best Local Similarity 87.8%; Pred. No. 3.8e-104;
Matches 455; Conservative 0; Mismatches 13; Indels 50; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTCTTCAGTTCTGTGTGGAGAC 60
Db 1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTCTTCAGTTCTGTGTGGAGAC 60

Qy 61 AGGGGCTTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG 120
Db 61 AGGGGCTTTTATTCAACAAGCCCACAGGATAACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy 121 ACAGGCATCGTGGATGAGTGTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
Db 121 ACAGGCATCGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy 181 TGCGCACCCCTCAAGCCTGCCAACGTCAGCTCGCTCTGTCCCGTCCCCAGCGCCACACCGAC 240
Db 181 TGTGCACCCCTCAAGCCGGAAAGGCAGCCCCCTCCGTCCCCAGCGCCACACCGAC 240

Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
Db 241 ATGCCCAAGACTCAG----- 255

Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
Db 256 ---AAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 311

Qy 361 GATGTA-GAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC 419
Db 312 GATGTAGGAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC 371

Qy 420 TGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTCAA 479
Db 372 TGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTCAA 431

Qy 480 AGATGGCATTCCCCAATGAAATACACAAGTAAACAT 517
Db 432 AGATGGCATTCCCCAATGAAATACACAAGTAAACAT 469

RESULT 7

AAS16884

ID AAS16884 standard; cDNA; 471 BP.

XX

AC AAS16884;

XX

DT 25-FEB-2002 (first entry)

XX

DE Rabbit insulin-like growth factor I liver-type isoform (L. IGF-I) cDNA.

XX

KW Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;

KW muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;
KW nerve avulsion; insulin-like growth factor I liver-type isoform; L.IGF-I;
XX
OS Oryctolagus cuniculus.
XX
FH Key Location/Qualifiers
FT CDS 1..318
FT /*tag= a
FT /product= "Rabbit L.IGF-I"
FT /partial
FT /note= "No start codon"
FT exon 1..75
FT /*tag= b
FT /number= exon 3
FT exon 76..258
FT /*tag= c
FT /number= exon 4
FT exon 259..315
FT /*tag= d
FT /number= exon 6
XX
PN WO200185781-A2.
XX
PD 15-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-GB02054.
XX
PR 10-MAY-2000; 2000GB-0011278.
XX
PA (UNLO) UNIV COLLEGE LONDON.
PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
XX
PI Goldspink G, Terenghi G;
XX
DR WPI; 2002-055585/07.
DR P-PSDB; AAU10564.
XX
PT Use of insulin-like growth factor I (IGF-I) isoform known as
PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT ability to reduce motoneuron loss in response to nerve avulsion, to
PT treat nerve damage
XX
PS Disclosure; Fig 10; 65pp; English.
XX
CC The invention relates to the use of an insulin-like growth factor I
CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC of a medicament for treating nerve damage in the peripheral nervous
CC system, or for treating nerve damage by localising MGF at the site of
CC damage. The nerve damage may include severing of a nerve. The treatment
CC may be combined with another treatment (such as a polypeptide growth
CC factor other than MGF) that prevents or diminishes degeneration of the
CC target organ (for example, muscle) which the damaged nerve innervates,
CC whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC MGF prevents or diminishes degeneration. The method is useful for
CC treating neurological disorders, preferably motorneuron disorders. These
CC methods can reduce motoneuron loss by 20% or greater in response to nerve
CC avulsion. This sequence represents cDNA encoding the rabbit insulin-like

CC growth factor I liver-type isoform (L.IGF-I) used in experiments on
 CC motoneuron loss.
 XX
 SQ Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;

 Query Match 73.0%; Score 377.2; DB 24; Length 471;
 Best Local Similarity 87.8%; Pred. No. 3.8e-104;
 Matches 455; Conservative 0; Mismatches 13; Indels 50; Gaps 2;

 QY 1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTCTTCAGTTCTGTGTGGAGAC 60
 |||||||
 Db 1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTCTTCAGTTCTGTGTGGAGAC 60

 QY 61 AGGGGCTTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
 |||||||
 Db 61 AGGGGCTTTTATTCAACAAGCCCACAGGATACTGGCTCCAGCAGTCGGAGGGCACCTCAG 120

 QY 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
 |||||||
 Db 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

 QY 181 TGCGCACCCCTCAAGCCTGCCAACGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
 |||
 Db 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240

 QY 241 ATGCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
 |||
 Db 241 ATGCCAAGACTCAG----- 255

 QY 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
 |||
 Db 256 ---AAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 311

 QY 361 GATGTA-GAAGACCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC 419
 |||
 Db 312 GATGTAGGAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC 371

 QY 420 TGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTCAA 479
 |||
 Db 372 TGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTCAA 431

 QY 480 AGATGGCATTCCCCAATGAAATACACAAGTAAACAT 517
 |||
 Db 432 AGATGGCATTCCCCAATGAAATACACAAGTAAACAT 469

RESULT 8

AAN70436

ID AAN70436 standard; cDNA; 818 BP.

XX

AC AAN70436;

XX

DT 25-MAR-2003 (updated)

DT 05-APR-1991 (first entry)

XX

DE Sequence encoding insulin-like growth factor 1A (IGF-1A).

XX

KW Growth promoter; lactation enhancer; cell proliferation; ss.
XX
OS Homo sapiens.
XX
PN EP229750-A.
XX
PD 22-JUL-1987.
XX
PF 06-JAN-1987; 87EP-0870001.
XX
PR 20-NOV-1986; 86US-0929671.
PR 07-JAN-1986; 86US-0816662.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Krivi GG, Rotwein PS;
XX
DR WPI; 1987-200203/29.
XX
PT New pre-pro-insulin-like growth factor-1 protein - obtd. by
PT recombinant DNA procedures for use as growth promoters for
PT enhancing lactation, for stimulating cell proliferation etc.
XX
PS Example; Fig 5; 59pp; English.
XX
CC A 42 base oligonucleotide corresponding to the DNA sequence encoding
CC amino acids 10 to 23 of mature human IGF-I was synthesized (AAN70437).
CC The radiolabeled 42 mer was then employed to screen for IGF-I
CC containing DNA sequences in a human liver cDNA library. Insulin-
CC like growth factors-1A and -1B cDNAs were isolated from a human cDNA
CC library by using lambda 11 (AAN70435, AAN70436). The human IGF-1
CC genomic gene was isolated and mapped. It encodes at least two
CC preproinsulin-like growth factor-1 proteins. An essentially pure
CC proproinsulin-like growth factor-1 protein comprising the sequence
CC of amino acids shown in Figure six is claimed (AAP70277).
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 818 BP; 232 A; 186 C; 187 G; 213 T; 0 other;

Query Match 66.6%; Score 344.2; DB 8; Length 818;
Best Local Similarity 87.3%; Pred. No. 4.8e-94;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy 1 GGACCGGAGACGCTCTGGGGCTGAGCTGGATGCTTCAGTTCTGTGTGGAGAC 60
|||
Db 203 GGACCGGAGACGCTCTGGGGCTGAGCTGGATGCTTCAGTTCTGTGTGGAGAC 262

Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 120
|||
Db 263 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 322

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
|||
Db 323 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 382

Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
|||

Db 383 TCGCACCCTCAAGCCTGCCAAGTCAGCTCGCTGTCCGTGCCAGGCCACACCGAC 442
 Qy 241 ATGCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
 |||||
 Db 443 ATGCCAAGACCCAG----- 457
 |||||
 Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
 |||||
 Db 458 ---AAGGAAGTACATTGAAGAACCGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 513
 |||||
 Qy 361 GATGTA-GAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC 419
 |||||
 Db 514 GATGTAGGAAGACCCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC 573
 |||||
 Qy 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC 477
 |||||
 Db 574 TGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTGATAACATTAA 633
 |||||
 Qy 478 AAAGAT-GGCATTTCCCCAATGAAATACACAAGTAAACAT 517
 |||||
 Db 634 AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT 674

RESULT 9

ABT11091

ID ABT11091 standard; cDNA; 7260 BP.

XX

AC ABT11091;

XX

DT 04-DEC-2002 (first entry)

XX

DE Human breast cancer associated coding sequence SEQ ID NO: 1225.

XX

KW Human; breast specific gene; breast cancer; differential expression;

KW cytostatic; gene therapy; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200259271-A2.

XX

PD 01-AUG-2002.

XX

PF 25-JAN-2002; 2002WO-US02176.

XX

PR 25-JAN-2001; 2001US-263757P.

PR 25-APR-2001; 2001US-286090P.

PR 23-MAY-2001; 2001US-292517P.

XX

PA (GENE-) GENE LOGIC INC.

XX

PI Orr MS, Nation M, Diggans JC, Zeng W;

XX

DR WPI; 2002-674803/72.

XX

PT Diagnosing breast cancer in a patient comprises detecting the level of

PT gene expression in cell or tissue samples, where a differential gene

PT expression is indicative of breast cancer

XX

PS Claim 1; SEQ ID NO 1225; 260pp + Sequence Listing; English.

XX

CC The present invention relates to methods of diagnosing breast cancer in a
CC patient, which comprise detecting the level of expression in a tissue
CC sample of two or more genes selected from those shown in ABT09867-
CC ABT11112, where a differential expression of the genes indicates breast
CC cancer. The methods are useful in diagnosing, treating, detecting the
CC progression, and in monitoring treatment of breast cancer in patients.
CC The methods are also useful as a screening tool for agents that modulate
CC the onset or progression of breast cancer. The breast cancer genes may be
CC used as diagnostic markers for the prediction or identification of the
CC malignant state of breast tissue, for confirming the type and progression
CC of cancer, and for drug screening and assays. The present sequence is a
CC coding sequence of the invention.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp://wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 66.6%; Score 344.2; DB 24; Length 7260;
Best Local Similarity 87.3%; Pred. No. 1.1e-93;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy 1 GGACCGGAGACGCTCTGGGGCTGAGCTGGATGCTTCAGTCGTGTGGAGAC 60
Db 311 GGACCGGAGACGCTCTGGGGCTGAGCTGGATGCTTCAGTCGTGTGGAGAC 370

Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG 120
Db 371 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG 430

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
Db 431 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCGTGCCAGCGCCACACCGAC 240
Db 491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCGTGCCAGCGCCACACCGAC 550

Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
Db 551 ATGCCCAAGACCCAG----- 565

Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
Db 566 ----AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 621

Qy 361 GATGTA-GAAGACCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTGCTC 419
Db 622 GATGTTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC 681

Qy 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC 477
Db 682 TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTAA 741

Qy 478 AAAGAT-GGCATTTCCCCAATGAAATACACAAGTAAACAT 517
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 742 AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT 782

RESULT 10

ABK84583

ID ABK84583 standard; cDNA; 7260 BP.

XX

AC ABK84583;

XX

DT 14-AUG-2002 (first entry)

XX

DE Human cDNA differentially expressed in granulocytic cells #1154.

XX

KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.

XX

OS Homo sapiens.

XX

PN WO200228999-A2.

XX

PD 11-APR-2002.

XX

PF 03-OCT-2001; 2001WO-US30821.

XX

PR 03-OCT-2000; 2000US-237189P.

XX

PA (GENE-) GENE LOGIC INC.

XX

PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX

DR WPI; 2002-435328/46.

XX

PT Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -

XX

PS Claim 1; SEQ ID No 1154; 114pp; English.

XX

CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the

CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp://wipo.int/pub/published_pct_sequences.

xx SO Sequence 7260 BP: 3330 A: 1415 G: 1340 C: 2275 T: 93 others

Query Match 66.6%; Score 344.2; DB 24; Length 7260;
Best Local Similarity 87.3%; Pred. No. 1.1e-93;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGAC 60

Db 311 GGACCGGAGACGCTCTGGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC 370

371 AGCCCCCTTTATTTCAAGAACGGCCAGGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 120
Pb

...TACCGCTTATGGCTCCAGGAGTCGGAGGGGGCTTAG 430

Pb 431 ACAGGGCATCGTGGATGACTGCTGCTTCGGGAGCTGTATCTAACCGACCCCTCCAGATCTAT 180

Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTGTCCGTGCCAGCGCCACACCGAC 240

Db 491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTGTCCGTGCCAGCGCCACACCGAC 550

351 ATGCCCAAGACCCAG----- 565
361 AGGNNAGGAGCTGATTTGGTGTG

Db 566 ---AAGGAAGTACATTGAAAGAACGCAAGTAGAGGGAGTCAGGAAACAAGAACTACAG 621

Qy 361 GATGTA-GAAGACCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTGCTC 419
||| ||| ||| ||| |||
Db 622 GATGTAGGAAGACCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC 681
||| ||| ||| ||| |||
Qy 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC 477
||| ||| ||| ||| |||
Db 682 TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTAA 741
||| ||| ||| |||
Qy 478 AAAGAT-GGCATTTCCCCAATGAAATACACAAGTAAACAT 517
||| ||| ||| ||| |||
Db 742 AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT 782

RESULT 11

ABN97244

ID ABN97244 standard; DNA; 7260 BP.

XX

AC ABN97244;

XX

DT 13-AUG-2002 (first entry)

XX

DE Gene #3742 used to diagnose liver cancer.

XX

KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.

XX

OS Homo sapiens.

XX

PN WO200229103-A2.

XX

PD 11-APR-2002.

XX

PF 02-OCT-2001; 2001WO-US30589.

XX

PR 02-OCT-2000; 2000US-237054P.

XX

PA (GENE-) GENE LOGIC INC.

XX

PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

XX

DR WPI; 2002-426119/45.

XX

PT Diagnosing and detecting the progression of liver cancer,
PT hepatocellular carcinoma or metastatic liver tumor in a patient,
PT involves detecting the level of expression of two or more genes in a
PT liver tissue sample -

XX

PS Claim 1; SEQ ID NO 3742; 298pp; English.

XX

CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting

CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pct_sequences](ftp://wipo.int/pub/published_pct_sequences).

XX

SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 66.6%; Score 344.2; DB 24; Length 7260;
Best Local Similarity 87.3%; Pred. No. 1.1e-93;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy 1 GGACCGGAGACGCTCTGGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC 60
Db 311 GGACCGGAGACGCTCTGGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC 370

Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG 120
Db 371 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG 430

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
Db 431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
Db 491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550

Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
Db 551 ATGCCCAAGACCCAG----- 565

Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
Db 566 ---AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 621

Qy 361 GATGTA-GAAGACCCCTCTGAGGAGTGAAGAAGAACAGGGCCACCGCAGGACCCCTTGCTC 419
Db 622 GATGTAGGAAGACCCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC 681

Qy 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC 477
Db 682 TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTTC 741

Qy 478 AAAGAT-GGCATTCCCCAATGAAATACACAAGTAAACAT 517
Db 742 AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT 782

RESULT 12

ABK64812

ID ABK64812 standard; DNA; 7260 BP.

XX

AC ABK64812;

XX
DT 18-JUN-2002 (first entry)
XX
DE Human benign prostatic hyperplasia gene #707.
XX
KW Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200212440-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-US24708.
XX
PR 07-AUG-2000; 2000US-223323P.
PR 05-JUN-2001; 2001US-0873319.
XX
PA (GENE-) GENE LOGIC INC.
PA (NISB) JAPAN TOBACCO INC.
XX
PI Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;
XX
DR WPI; 2002-257476/30.
XX
PT Identifying drugs for and diagnosing benign prostatic hyperplasia, by
PT detecting expression levels of one or more genes in prostate cells from
PT patient that are differentially regulated compared to normal prostate
PT cells -
XX
PS Disclosure; Page 391-393; 444pp; English.
XX
CC The invention relates to a method of diagnosing (I) the onset or
CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
CC or identifying an agent that modulates the onset or progression of BPH.
CC The method is based on changes in gene expression in BPH tissue isolated
CC from patients exhibiting different clinical states of prostate
CC hyperplasia as compared to normal prostate tissue. (I) comprises
CC detecting the expression levels of one or more genes in prostate cells
CC from the subject that are differentially regulated compared to normal
CC prostate cells. (II) comprises preparing a first gene expression profile
CC of BPH cells or BPH-like cell population, exposing the cells to the
CC agent, preparing a second gene expression profile of the agent exposed
CC cells, and comparing the first and second gene expression profiles.
CC (I) is useful for diagnosing the onset or progression of BPH. (II) is
CC useful for identifying an agent that modulates the onset or progression
CC of BPH. The methods are useful to present information identifying
CC the expression level in a tissue or cells, by comparing the expression
CC level of genes given in the specification in the tissue or cells to the
CC level of expression of gene in the database, and displaying the
CC expression levels of at least one gene in the tissue or cell sample
CC compared to the expression level in BPH. Agents using (II) are useful for
CC treating BPH or prostate cancer. ABK64106-ABK64860 represent human
CC benign prostatic hyperplasia gene sequences of the invention.
XX
SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 66.6%; Score 344.2; DB 24; Length 7260;
 Best Local Similarity 87.3%; Pred. No. 1.e-93;
 Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy	1	GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTCTTCAGTCGTGTGGAGAC	60
Db	311	GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTCTTCAGTCGTGTGGAGAC	370
Qy	61	AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG	120
Db	371	AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG	430
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	431	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	490
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240
Db	491	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	550
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA	300
		-----	-----
Db	551	ATGCCCAAGACCCAG-----	565
	-----	-----	-----
Qy	301	AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	360
Db	566	---AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	621
	---	-----	-----
Qy	361	GATGTA-GAACACCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTGCTC	419
Db	622	GATGTAGGAAGACCCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC	681
Qy	420	TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC	477
Db	682	TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTTC	741
	-----	-----	-----
Qy	478	AAAGAT-GGCATTCCCCAATGAAATACACAAGTAAACAT	517
Db	742	AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT	782
	-----	-----	-----

RESULT 13

ABK35504

ID ABK35504 standard; DNA; 7260 BP.

XX

AC ABK35504;

XX

DT 08-MAY-2002 (first entry)

XX

DE Human endometrial cancer related gene, IGF1.

XX

KW Human; ds; gene; endometrial cancer; differential expression;
KW DNA microarray; protein microarray.

XX

OS Homo sapiens.

XX

PN WO200209573-A2.

XX
PD 07-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-US24104.
XX
PR 31-JUL-2000; 2000US-221735P.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX
PI Mutter GL;
XX
DR WPI; 2002-179967/23.
DR P-PSDB; AAU84284.
XX
PT Diagnosing endometrial cancer comprises determining expression of
PT nucleic acid molecules or expression products that are differentially
PT expressed in normal and malignant endometrium -
XX
PS Claim 1; Page 85-89; 233pp; English.
XX
CC The invention relates to diagnosing endometrial cancer in a subject
CC suspected of having endometrial cancer comprising determining the
CC expression of a set of nucleic acid molecules or expression products in
CC an endometrial sample suspected of being cancerous, where the set of
CC nucleic acid molecules comprises at least 2 nucleic acid molecules
CC selected from 50 fully defined sequences as given in the specification.
CC The nucleic acids are used as an array of at least 2 of the 50
CC nucleic acids bound to a solid substrate. Also included is a solid-phase
CC protein microarray comprising at least 2 antibodies or its antigen
CC binding fragments, that specifically bind at least 2 different
CC polypeptides from the 50 fully defined sequences as given in the
CC specification, fixed to a solid substrate. The methods and arrays are
CC useful for the diagnosis of endometrial cancer, selecting and monitoring
CC treatment regimes and identification of lead compounds useful for the
CC treatment of endometrial cancer. The present sequence is one of 50
CC genes differentially expressed between cancerous and non-cancerous
CC samples.
XX
SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 66.6%; Score 344.2; DB 24; Length 7260;
Best Local Similarity 87.3%; Pred. No. 1.1e-93;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy 1 GGACCGGAGACGCTCTGGGGCTGAGCTGGATGCTTCAGTCGTGTGGAGAC 60
|||
Db 311 GGACCGGAGACGCTCTGGGGCTGAGCTGGATGCTTCAGTCGTGTGGAGAC 370

Qy 61 AGGGGTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 120
|||
Db 371 AGGGGTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 430

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
|||
Db 431 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTGTCCGTGCCAGCGCCACACCGAC 240

Db	491	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGGCCACACCGAC	550
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA	300
Db	551	ATGCCCAAGACCCAG-----	565
Qy	301	AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	360
Db	566	---AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	621
Qy	361	GATGTA-GAAGACCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC	419
Db	622	GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC	681
Qy	420	TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC	477
Db	682	TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTAA	741
Qy	478	AAAGAT-GGCATTCCCCAATGAAATACACAAGTAAACAT	517
Db	742	AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT	782

RESULT 14

ABK35561

ID ABK35561 standard; DNA; 7260 BP.

XX

AC ABK35561;

XX

DT 08-MAY-2002 (first entry)

XX

DE Gene IGF1 differentially expressed in breast cancer tissue.

XX

KW Human; diagnosis of breast cancer; endometrial cancer; breast tumour;

KW MAI; mitotic activity index; cytostatic; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200210436-A2.

XX

PD 07-FEB-2002.

XX

PF 27-JUL-2001; 2001WO-US23642.

XX

PR 28-JUL-2000; 2000US-222093P.

XX

PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.

PA (BAAK/) BAAK J.

XX

PI Baak J, Mutter GL;

XX

DR WPI; 2002-180084/23.

DR P-PSDB; AAU84341.

XX

PT Diagnosing breast cancer comprises determining expression of nucleic acid molecules or expression products that are differentially expressed

PT in normal and malignant tissue -

XX

PS Claim 1; Page 74-78; 219pp; English.

XX

CC The present invention relates to a method for diagnosing breast cancer
CC in a subject suspected of having endometrial cancer. The method
CC comprises determining the expression of a set of human genes or
CC expression products in an endometrial sample suspected of being
CC cancerous. The human genes of the invention are differentially
CC expressed in breast tumours characterised as high or low MAI (mitotic
CC activity index). These sets of genes can be used to discriminate between
CC high and low MAI breast tumours. The invention also provides DNA and
CC protein microarrays for analysing the expression of the human genes and
CC their protein products. The methods and arrays are useful for the
CC diagnosis and prognosis of endometrial cancer, selecting and monitoring
CC treatment regimes, and identification of compounds useful for the
CC treatment of endometrial cancer. ABK35531-ABK35581 represent the human
CC genes of the invention that are differentially expressed in breast
CC cancer tissue.

XX

SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 66.6%; Score 344.2; DB 24; Length 7260;
Best Local Similarity 87.3%; Pred. No. 1.1e-93;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy	1	GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTTCAGTTCTGTGTGGAGAC	60
Db	311	GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTTCAGTTCTGTGTGGAGAC	370
Qy	61	AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG	120
Db	371	AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG	430
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	431	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	490
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240
Db	491	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	550
Qy	241	ATGCCCAAGACCCAGAACGACTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA	300
Db	551	ATGCCCAAGACCCAG-----	565
Qy	301	AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	360
Db	566	---AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	621
Qy	361	GATGTA-GAACGCCCTCTGAGGAGTGAAGAACAGGACAGGCCACCGCAGGACCCTTGCTC	419
Db	622	GATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC	681
Qy	420	TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC	477
Db	682	TGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTGATAACATTAA	741

QY 478 AAAGAT-GGCATTTCCCCAATGAAATACACAAGTAAACAT 517
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 742 AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT 782

RESULT 15

AAT84894

ID AAT84894 standard; cDNA; 777 BP.

XX

AC AAT84894;

XX

DT 14-APR-1998 (first entry)

XX

DE Human insulin like growth factor 1 Ea isoform encoding cDNA.

XX

KW Insulin like growth factor 1; IGF-1; Ec peptide; muscle disorder;
KW heart; neuromuscular disease; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 26..496

FT /*tag= a

FT /product= "IGF-1 Ea isoform"

XX

PN WO9733997-A1.

XX

PD 18-SEP-1997.

XX

PF 11-MAR-1997; 97WO-GB00658 .

XX

PR 11-MAR-1996; 96GB-0005124 .

XX

PA (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.

XX

PI Goldspink G;

XX

DR WPI; 1997-470877/43 .

DR P-PSDB; AAW23302 .

XX

PT Use of insulin like growth factor I characterised by presence of Ec
PT peptide - to treat humans or animals, particularly muscle disorders,
PT heart conditions or neuromuscular diseases

XX

PS Disclosure; Fig 4; 33pp; English.

XX

CC A use of insulin like growth factor I (IGF-1) has been developed, and
CC is characterised by the presence of the Ec peptide, or a functional
CC equivalent, in the treatment or therapy of a human or animal. The IGF-1
CC polypeptide can be used to treat muscular disorders, e.g. Duchenne or
CC Becker muscular dystrophy, autosomal dystrophies and related progressive
CC skeletal muscle weakness and wasting, muscle atrophy in ageing humans,
CC spinal cord injury induced muscle atrophy and neuromuscular diseases,
CC and cardiac disorders, e.g. diseases where promotion of cardiac muscle
CC protein synthesis is a beneficial treatment, cardiomyopathies and acute
CC heart failure or insult, specifically myocarditis or myocardial

CC infarction. It can also be used to promote bone fracture healing and
CC maintenance of bone in old age. The present sequence encodes human
CC IGF-1 Ea isoform used in the present specification.

XX

SQ Sequence 777 BP; 201 A; 193 C; 204 G; 179 T; 0 other;

Query Match 66.3%; Score 342.6; DB 18; Length 777;
Best Local Similarity 87.1%; Pred. No. 1.4e-93;
Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;

Qy 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTCTTCAGTCGTGTGGAGAC 60
Db 179 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTCTTCAGTCGTGTGGAGAC 238

Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
Db 239 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 298

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
Db 299 ACAGGTATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 358

Qy 181 TGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
Db 359 TGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 418

Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
Db 419 ATGCCCAAGACCCAG----- 433

Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
Db 434 ---AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 489

Qy 361 GATGTA-GAACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTGCTC 419
Db 490 GATGTAGGAAGACCCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC 549

Qy 420 TGCAC-AGTTACCTG-TAAACATTGAAATACCGGCCAAAAATAAGTTGATCACATTTC 477
Db 550 TGCACGAGTTACCTGTTAAACTTGAAACACCTACCAAAAAATAAGTTGATAACATTAA 609

Qy 478 AAAGAT-GGCATTCCCCAATGAAATAACACAAGTAAACAT 517
Db 610 AAAGATGGCGTTCCCCAATGAAATAACACAAGTAAACAT 650

Search completed: December 13, 2003, 06:03:48
Job time : 209.586 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 06:03:55 ; Search time 47.8037 Seconds
(without alignments)
4773.589 Million cell updates/sec

Title: US-09-852-261-1

Perfect score: 517

Sequence: 1 ggaccggagacgctctgcgg.....tgaaatacacaagtaaacat 517

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	467.4	90.4	553	3	US-09-142-583A-3	Sequence 3, Appli
2	467.4	90.4	553	3	US-09-142-583A-5	Sequence 5, Appli
3	342.6	66.3	777	3	US-09-142-583A-10	Sequence 10, Appli
4	339.4	65.6	622	6	5405942-2	Patent No. 5405942
5	286.4	55.4	5707	2	US-08-472-809B-8	Sequence 8, Appli
6	286.4	55.4	6345	2	US-08-472-809B-7	Sequence 7, Appli
7	255.2	49.4	357	6	5405942-13	Patent No. 5405942
8	253.6	49.1	357	6	5405942-9	Patent No. 5405942
9	208.4	40.3	210	6	5405942-7	Patent No. 5405942
10	208.4	40.3	210	6	5405942-11	Patent No. 5405942
11	208.4	40.3	2862	4	US-09-255-829-13	Sequence 13, Appli

12	206.8	40.0	210	6	5405942-15	Patent No. 5405942	
13	202.8	39.2	240	1	US-08-308-196A-1	Sequence 1, Appli	
14	202.8	39.2	240	5	PCT-US91-06452-1	Sequence 1, Appli	
15	202.8	39.2	390	3	US-09-029-267-13	Sequence 13, Appl	
16	174.4	33.7	798	1	US-07-953-230A-6	Sequence 6, Appli	
17	163.4	31.6	770	1	US-07-953-230A-1	Sequence 1, Appli	
18	163.4	31.6	846	1	US-07-953-230A-5	Sequence 5, Appli	
19	125.8	24.3	485	1	US-07-989-845-29	Sequence 29, Appli	
20	125.8	24.3	485	1	US-07-989-844-13	Sequence 13, Appli	
21	125.8	24.3	485	1	US-08-110-663-1	Sequence 1, Appli	
22	125.8	24.3	485	1	US-08-169-688-1	Sequence 1, Appli	
23	125.8	24.3	485	1	US-08-240-121-13	Sequence 13, Appli	
24	125.8	24.3	485	1	US-08-451-241-13	Sequence 13, Appli	
25	125.8	24.3	485	1	US-08-110-664-1	Sequence 1, Appli	
26	125.8	24.3	485	1	US-08-446-882-1	Sequence 1, Appli	
27	125.8	24.3	485	1	US-08-385-187A-1	Sequence 1, Appli	
28	125.8	24.3	485	1	US-08-470-108-1	Sequence 1, Appli	
29	125.8	24.3	485	5	PCT-US93-11297-13	Sequence 13, Appli	
30	125.8	24.3	485	5	PCT-US93-11298-29	Sequence 29, Appli	
31	123.8	23.9	621	3	US-08-989-251-40	Sequence 40, Appli	
32	123.8	23.9	621	3	US-09-340-250-40	Sequence 40, Appli	
33	123.8	23.9	621	4	US-09-528-108-40	Sequence 40, Appli	
34	122	23.6	237	1	US-07-764-655D-8	Sequence 8, Appli	
35	120.8	23.4	243	2	US-08-482-182-75	Sequence 75, Appli	
36	120.4	23.3	233	1	US-08-444-142-3	Sequence 3, Appli	
37	120.4	23.3	233	1	US-08-444-131-3	Sequence 3, Appli	
C	38	120.4	23.3	237	1	US-07-764-655D-9	Sequence 9, Appli
39	120.4	23.3	717	1	US-08-284-784-40	Sequence 40, Appli	
40	120.4	23.3	717	2	US-08-854-811-40	Sequence 40, Appli	
41	120.4	23.3	783	1	US-08-284-784-43	Sequence 43, Appli	
42	120.4	23.3	783	2	US-08-854-811-43	Sequence 43, Appli	
43	120.4	23.3	891	1	US-08-284-784-33	Sequence 33, Appli	
44	120.4	23.3	891	1	US-08-284-784-34	Sequence 34, Appli	
45	120.4	23.3	891	2	US-08-854-811-33	Sequence 33, Appli	

ALIGNMENTS

RESULT 1

US-09-142-583A-3

; Sequence 3, Application US/09142583A

; Patent No. 6221842

; GENERAL INFORMATION:

; APPLICANT: GOLDSPIK, GEOFFREY

; TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,583A
FILING DATE: 29-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB97/00658
FILING DATE: 11-MAR-1997
APPLICATION NUMBER: GB 9605124.8
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 117-263
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..363
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-142-583A-3

Query Match 90.4%; Score 467.4; DB 3; Length 553;
Best Local Similarity 96.2%; Pred. No. 1.2e-134;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 31 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC 90
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 61 AGGGGCTTTATTCACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCCCTCAG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 91 AGGGGCTTTATTCACAAGCCCACAGGATAACGGCTCCAGCAGTCGGAGGGCACCTCAG 150
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 151 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCTGCCAGCGCCACACCGAC 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 211 TGTGCACCCCTCAAGCCGGAAAGGCAGGCCCTCCGTCGTGCCAGCGCCACACCGAC 270
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 271 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 330
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 298 AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 331 AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390
Qy 358 CAGGATGTA-GAAGACCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 416
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 391 CAGGATGTAGGAAGACCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 450
Qy 417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTT 476
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 451 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTT 510
Qy 477 CAAAGATGGCATTTCCCCAATGAAATACACAAGTAAACAT 517
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 511 CAAAGATGGCATTTCCCCAATGAAATACACAAGTAAACAT 551

RESULT 2

US-09-142-583A-5

; Sequence 5, Application US/09142583A

; Patent No. 6221842

; GENERAL INFORMATION:

; APPLICANT: GOLDSPINK, GEOFFREY

; TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/142,583A

; FILING DATE: 29-Oct-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/GB97/00658

; FILING DATE: 11-MAR-1997

; APPLICATION NUMBER: GB 9605124.8

; FILING DATE: 11-MAR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: SADOFF, B. J.

; REGISTRATION NUMBER: 36663

; REFERENCE/DOCKET NUMBER: 117-263

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 7038164000

; TELEFAX: 7038164100

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 553 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: linear

MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 341..397
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-142-583A-5

Query Match 90.4%; Score 467.4; DB 3; Length 553;
Best Local Similarity 96.2%; Pred. No. 1.2e-134;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTCTTCAGTTCTGTGTGGAGAC 60
Db 31 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTCTTCAGTTCTGTGTGGAGAC 90

Qy 61 AGGGGCTTITATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 120
Db 91 AGGGGCTTTATTCAACAAGCCCACAGGATACTGGCTCCAGCAGTCGGAGGGCACCTCAG 150

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
Db 151 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210

Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGGCCACACCGAC 240
Db 211 TGTGCACCCCTCAAGCCGGCAAGGCAGGCCCTCGTCCGTGCCAGGCCACACCGAC 270

Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
Db 271 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAATGAAGTCTCAGAGG 330

Qy 298 AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
Db 331 AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390

Qy 358 CAGGATGTA-GAAGACCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 416
Db 391 CAGGATGTAGGAAGACCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 450

Qy 417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATT 476
Db 451 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATT 510

Qy 477 CAAAGATGGCATTCCCCAATGAAATACACAAGTAAACAT 517
Db 511 CAAAGATGGCATTCCCCAATGAAATACACAAGTAAACAT 551

RESULT 3

US-09-142-583A-10

; Sequence 10, Application US/09142583A

Patent No. 6221842

GENERAL INFORMATION:

APPLICANT: GOLDSPIK, GEOFFREY

TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS

TYPE OF INVENTION: MET
NUMBER OF SEQUENCES: 11

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/142,583A
FILING DATE: 29-Oct-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION DATA
APPLICATION NUMBER: WO PCT/GB97/00658
FILING DATE: 11-MAR-1997
APPLICATION NUMBER: GB 9605124.8
FILING DATE: 11-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36663
REFERENCE/POCKET NUMBER: 117-262

REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION

TELEPHONE: 7038164000
FAX: 7038164100

TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 10

SEQUENCE CHARACTERISTICS

ENCE CHARACTERISTICS:
LENGTH: 777 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear

MOLECULE TYPE: cDNA

NAME/KEY: CDS
LOCATION: 65 ABC

LOCATION: 26..493

; SEQUENCE

Query Match 66.3%; Score 342.6; DB 3; Length 777;
Best Local Similarity 87.1%; Pred. No. 4.4e-96;
Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;

Qy 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTCTTCAGTCGTGTGGAGAC 60

Cy 61 AGCGCCCTTATTCGAGAAGAAGGGAGACGGTATGGCTGAGCTGGTGGAATGCTTCAGTTCTGCTGGAGAC 120

Db 239 AGGGGCTTTATTCACAAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 298

QY 121 ACAGGGCATCGTGGAATGAGTGCCTCCGGAGCTGTGATCTAAGGAGGGCTGGAGATGTAT 180
E 200

181 TCCGGAGCCCTGAACCTGGCAACTGAGATCCCTCTCTACCTACGGAGCCCCAGCCCCAG 318

Db	359	TGCCCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGGCCACACCGAC	418
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA	300
Db	419	ATGCCCAAGACCCAG-----	433
Qy	301	AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	360
Db	434	---AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	489
Qy	361	GATGTA-GAAGACCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC	419
Db	490	GATGTAGGAAGACCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC	549
Qy	420	TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC	477
Db	550	TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTAA	609
Qy	478	AAAGAT-GGCATTTCCCCAATGAAATAACACAAGTAAACAT	517
Db	610	AAAGATGGCGTTCCCCAATGAAATAACACAAGTAAACAT	650

RESULT 4

5405942-2

; Patent No. 5405942

; APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,

; JAMES P.

; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS

; I AND II

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/65,673

; FILING DATE: 16-JUN-1987

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 630,557

; FILING DATE: 19-JUL-1984

; SEQ ID NO:2:

; LENGTH: 622

5405942-2

Query Match	65.6%	Score 339.4;	DB 6;	Length 622;
Best Local Similarity	69.7%	Pred. No. 3.9e-95;		
Matches	363;	Conservative	89;	Mismatches 16; Indels 53; Gaps 5;
Qy	1	GGACCGGAGACGCTCTGGGGCTGAGCTGGTGGATGCTTCAAGTTCAGTGTGTGGAGAC	60	
Db	45	GGACCGGAGACGCUUGCGGGCUGAGCUGGUGGAUGCUCUUCAGUUCGUGUGUGGAGAC	104	
Qy	61	AGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG	120	
Db	105	AGGGCUUUUAUUCAACAAGCCCACAGGUUAUGGUCCAGCAGUCGGAGGGCGCCUCAG	164	
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180	
Db	165	ACAGGUAUUGGUGGAUGAGUGCUGCUUCCGGAGCUGUGAUCAUAGGAGGCUGGAGAUGUAU	224	

Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCGTGCCAGGCCACACCGAC 240
Db 225 UGCACCCCUCAAGCCUGCCAAGUCAGCUCGUCUGUCCGUGGCCAGCGCCACACCGAC 284

Qy 241 ATGCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
Db 285 AUGCCAAGACCCAG----- 299

Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
Db 300 ---AAGGAAGUACAUJUGAAGAACGCAAGUAGAGGGAGUGCAGGAAACAAGAACUACAG 355

Qy 361 GATGTA-GAAGACCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCTTGCTC 419
Db 356 GAUGUAGGAAGACCCUCCUGAGGAGUGAAGAGUGACAUGCACCGCAGGAUCCUUUGCUC 415

Qy 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC 477
Db 416 UGCACGAGUUACCUUAAAACUUGGAACACCUACCAAAAAAUAGUUUGAUACAUUA 475

Qy 478 AAAGAT-GGCATTCCCCAATGAAATACACAAGTAAACAT 517
Db 476 AAAGAUGGGCGUUUCCCCCAAUGAAAACACAAGUAAACAU 516

RESULT 5

US-08-472-809B-8

; Sequence 8, Application US/08472809B

; Patent No. 5925564

; GENERAL INFORMATION:

; APPLICANT: Schwartz, Robert J.

; APPLICANT: DeMayo, Franco J.

; APPLICANT: O'Malley, Bert W.

; TITLE OF INVENTION: Expression Vector Systems and

; TITLE OF INVENTION: Method of Use

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/472,809B

; FILING DATE: June 7, 1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/209,846

; FILING DATE: March 9, 1994
; APPLICATION NUMBER: 07/789,919
; FILING DATE: No. 5925564ember 6, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 214/212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5707 bases
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

US-08-472-809B-8

Query Match 55.4%; Score 286.4; DB 2; Length 5707;
Best Local Similarity 85.6%; Pred. No. 2.3e-78;
Matches 363; Conservative 0; Mismatches 11; Indels 50; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 793 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC 852
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 853 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG 912
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 913 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 972
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 181 TGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 973 TGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 1032
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
||| ||| ||| ||| |||
Db 1033 ATGCCCAAGACCCAG----- 1047
||| ||| ||| |||
Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
||| ||| ||| ||| |||
Db 1048 ---AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 1103
||| ||| ||| |||
Qy 361 GATGTA-GAACCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC 419
||| ||| ||| ||| |||
Db 1104 GATGTAGGAAGACCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCCCGGC 1163
||| ||| ||| |||
Qy 420 TGCA 423
|||
Db 1164 TGCA 1167

RESULT 6

US-08-472-809B-7

; Sequence 7, Application US/08472809B

; Patent No. 5925564

; GENERAL INFORMATION:

; APPLICANT: Schwartz, Robert J.

; APPLICANT: DeMayo, Franco J.

; APPLICANT: O'Malley, Bert W.

; TITLE OF INVENTION: Expression Vector Systems and

; TITLE OF INVENTION: Method of Use

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/472,809B

; FILING DATE: June 7, 1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/209,846

; FILING DATE: March 9, 1994

; APPLICATION NUMBER: 07/789,919

; FILING DATE: No. 5925564ember 6, 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 214/212

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6345 bases

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-472-809B-7

Query Match 55.4%; Score 286.4; DB 2; Length 6345;

Best Local Similarity 85.6%; Pred. No. 2.4e-78;

Matches 363; Conservative 0; Mismatches 11; Indels 50; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTTCAGTTCTGTGTGGAGAC 60

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 3702 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC 3761
 Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 120
 |||||
 Db 3762 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 3821
 |||||
 Qy 121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
 |||||
 Db 3822 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 3881
 |||||
 Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCAACCGAC 240
 |||||
 Db 3882 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCAACCGAC 3941
 |||||
 Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
 |||||
 Db 3942 ATGCCCAAGACCCAG----- 3956
 |||||
 Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
 |||||
 Db 3957 ---AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 4012
 |||||
 Qy 361 GATGTA-GAAGACCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC 419
 |||||
 Db 4013 GATGTAGGAAGACCCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCCCGGGC 4072
 |||||
 Qy 420 TGCA 423
 |||||
 Db 4073 TGCA 4076

RESULT 7

5405942-13

; Patent No. 5405942

; APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,
; JAMES P.

; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS

; I AND II

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/65,673

; FILING DATE: 16-JUN-1987

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 630,557

; FILING DATE: 19-JUL-1984

; SEQ ID NO:13:

; LENGTH: 357

5405942-13

Query Match 49.4%; Score 255.2; DB 6; Length 357;
 Best Local Similarity 98.8%; Pred. No. 2.8e-69;
 Matches 257; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC 60
 |||||

Db 43 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC 102
 |||||

Qy	61	AGGGGCTTTATTCACACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	120
Db	103	AGGGGCTTTATTCACACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	162
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	163	ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	222
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTGTCCGTGCCAGCGCCACACCGAC	240
Db	223	TGCGCACCCCTCAGGCCAGTCAGCTCGCTGTCCGTGCCAGCGCCACACCGAC	282
Qy	241	ATGCCCAAGACCCAGAAGTA	260
Db	283	ATGCCCAAGACCCAGAAGGA	302

RESULT 8

5405942-9

; Patent No. 5405942

APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,

JAMES P.

TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS

; I AND II

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/65,673

; FILING DATE: 16-JUN-1987

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 630,557

FILING DATE: 19-JUL-1984

;SEQ ID NO:9;

LENGTH: 357

5405942-9

Query Match 49.1%; Score 253.6; DB 6; Length 357;
Best Local Similarity 79.2%; Pred. No. 8.8e-69;

Qy	1	GGACCGGAGACGCTCTGCGGGCTGAGCTGGATGCTTCAGTTCGTGTGGAGAC	60
		: : : : : : : : : : : : :	
Db	43	GGACCGGAGACGCUCUGCGGGCUGAGCUGGUGGACGCUCUUCAGUUCGUGUGUGGAGAC	102

```

Qy          61 AGGGGCTTTATTCACAACAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTAG 120
           |||||::::|:||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db          103 AGGGCUUUUAUUCAACAAGCCCACAGGUUAUGGUCCAGCAGUCGGAGGGGCCUCAG 162

```

QY 181 TGCGCACCCCTCAAGCCCTGCCAAGTCAGCTCGCTCTGTCGGTGCCAGCGCCACACCGAC 240
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 223 UGCGCACCCCUCAAGCCUGCCAAGUCAGCUCGCUUCGUCCGUGGCCAGCGCCACACCGAC 282

Qy 241 ATGCCCAAGACCCAGAAGTA 260
| : | | | | | | | | | | | | | |

Db 283 AUGCCCAAGACCCAGAAGGA 302

RESULT 9

5405942-7

; Patent No. 5405942

; APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,
; JAMES P.

; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS

; I AND II

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/65,673

; FILING DATE: 16-JUN-1987

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 630,557

; FILING DATE: 19-JUL-1984

; SEQ ID NO:7:

; LENGTH: 210

5405942-7

Query Match 40.3%; Score 208.4; DB 6; Length 210;
Best Local Similarity 77.6%; Pred. No. 6e-55;
Matches 163; Conservative 46; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTCTTCAGTCGTGTGGAGAC 60
|||||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||

Db 1 GGACCGGAGACGCUUGCGGGCUGAGCUGGUGGAUGCUCUUCAGUUCGUGUGUGGAGAC 60

Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 120
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||

Db 61 AGGGGUUUUAUUCAAAGCCCACAGGGUAUGGCUCCAGCAGUCGGAGGGGCCUCAG 120

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||:|

Db 121 ACAGGUUAUCGUGGAUGAGUGCUGCUUCCGGAGCUGUGAUCAAGGAGGCUGGAGAUGUAU 180

Qy 181 TGCACCCCTCAAGCCTGCCAAGTCAGCT 210

:|||||:||||:||||:||||:||||

Db 181 UGCACCCCUAAGCCUGCCAAGUCAGCU 210

RESULT 10

5405942-11

; Patent No. 5405942

; APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,
; JAMES P.

; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS

; I AND II

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/65,673

; FILING DATE: 16-JUN-1987

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 630,557

; FILING DATE: 19-JUL-1984

; SEQ ID NO:11:

; LENGTH: 210

5405942-11

Query Match 40.3%; Score 208.4; DB 6; Length 210;
Best Local Similarity 99.5%; Pred. No. 6e-55;
Matches 209; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC 60

Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 ACAGGTATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCT 210
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCT 210

RESULT 11

US-09-255-829-13

; Sequence 13, Application US/09255829

; Patent No. 6461617

; GENERAL INFORMATION:

; APPLICANT: Shone, Clifford Charles

; APPLICANT: Quinn, Conrad Padraig

; APPLICANT: Foster, Keith Alan

; TITLE OF INVENTION: Recombinant Toxin Fragments

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/255,829

; FILING DATE: 23-FEB-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB97/02273

; FILING DATE: 22-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/782,893

; FILING DATE: 27-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: ESMOND, ROBERT W.

; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0130002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2862 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2862

US-09-255-829-13

Query Match 40.3%; Score 208.4; DB 4; Length 2862;
Best Local Similarity 99.5%; Pred. No. 1.9e-54;
Matches 209; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGAC 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2644 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGAC 2703

Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2704 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 2763

Qy 121 ACAGGCATCGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2764 ACAGGTATCGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 2823

Qy 181 TCGCACCCCTCAAGCCTGCCAAGTCAGCT 210
||| ||| ||| ||| ||| ||| ||| |||
Db 2824 TCGCACCCCTCAAGCCTGCCAAGTCAGCT 2853

RESULT 12

5405942-15

; Patent No. 5405942

; APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,
; JAMES P.

; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS

; I AND II

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/65,673

; FILING DATE: 16-JUN-1987

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 630,557

; FILING DATE: 19-JUL-1984

; SEQ ID NO: 15:

; LENGTH: 210

5405942-15

Query Match 40.0%; Score 206.8; DB 6; Length 210;

; REFERENCE/DOCKET NUMBER: 51875
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14..232

US-08-308-196A-1

Query Match 39.2%; Score 202.8; DB 1; Length 240;
Best Local Similarity 96.7%; Pred. No. 3.4e-53;
Matches 207; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy	1	GGACCGGAGACGCTCTGCAGGGCTGAGCTGGATGCTTCAGTCGTGTGGAGAC	60
Db	17	GGACCGGAGACGCTCTGCAGGGCTGAGCTCGTGGATGCTCTGCAGTCGTGTGGAGAC	76
Qy	61	AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG	120
Db	77	AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGACGGGCGCTCAG	136
Qy	121	ACAGGCATCGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	137	ACAGGCATCGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTCGAGATGTAT	196
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCT	214
Db	197	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT	230

RESULT 14

PCT-US91-06452-1
; Sequence 1, Application PC/TUS9106452
; GENERAL INFORMATION:
; APPLICANT: Brierley, Russell A.
; APPLICANT: Davis, Geneva R.
; APPLICANT: Holtz, Gregory C.
; APPLICANT: Gleeson, Martin A.
; APPLICANT: Bradley, D. H.
; TITLE OF INVENTION: Production of Insulin-Like Growth
; TITLE OF INVENTION: Factor-1 in Methylotrophic Yeast Cells
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 South LaSalle Street, Suite 900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/06452
; FILING DATE: 19910409
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/578,728
; FILING DATE: 04-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 51874
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)552-1311
; TELEFAX: (619)552-0095
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14..232

PCT-US91-06452-1

Query Match 39.2%; Score 202.8; DB 5; Length 240;
Best Local Similarity 96.7%; Pred. No. 3.4e-53;
Matches 207; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy	1	GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGAC	60
Db	17	GGACCGGAGACGCTCTGCGGGCTGAGCTCGTGGATGCTCTGCAGTCGTGTGGAGAC	76
Qy	61	AGGGGTTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	120
Db	77	AGGGGTTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGACGGCGCCTCAG	136
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	137	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTCGAGATGTAT	196
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCT	214
Db	197	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT	230

RESULT 15
US-09-029-267-13
; Sequence 13, Application US/09029267
; Patent No. 6107057
; GENERAL INFORMATION:
; APPLICANT: Crawford, Kenneth

; APPLICANT: Zaror, Isabel
; APPLICANT: Innis, Michael
; TITLE OF INVENTION: Pichia Secretory Leader for Protein
; TITLE OF INVENTION: Expression
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: United States
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/029,267
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Chung, Ling-Fong
; REGISTRATION NUMBER: 36,482
; REFERENCE/DOCKET NUMBER: 1165,100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2704
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic"
US-09-029-267-13

Query Match 39.2%; Score 202.8; DB 3; Length 390;
Best Local Similarity 96.7%; Pred. No. 4.2e-53;
Matches 207; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGGGGCTGAGCTGGATGCTCTCAGTCGTGTGGAGAC 60
Db 160 GGACCGGAGACGCTCTGGGGCTGAGCTGGATGCTCTCAGTCGTGTGGAGAC 219

Qy 61 AGGGGTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 120
Db 220 AGGGGTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGACGGGCGCTCAG 279

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
Db 280 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTCGAGATGTAT 339

Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCT 214
Db 340 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT 373

Search completed: December 13, 2003, 11:44:49
Job time : 49.8037 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 07:29:55 ; Search time 230.833 Seconds
(without alignments)
7443.919 Million cell updates/sec

Title: US-09-852-261-1
Perfect score: 517
Sequence: 1 ggaccggagacgctctgcgg.....tgaaaatacacaagtaaacat 517

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	%				
No.	Score	Match	Length	DB	ID	Description

1	517	100.0	517	9	US-09-852-261-1	Sequence 1, Appli	
2	467.4	90.4	523	9	US-09-852-261-5	Sequence 5, Appli	
3	377.2	73.0	471	9	US-09-852-261-13	Sequence 13, Appli	
4	344.2	66.6	7260	10	US-09-919-497-24	Sequence 24, Appli	
5	344.2	66.6	7260	10	US-09-880-107-3739	Sequence 3739, Ap	
6	344.2	66.6	7260	13	US-09-873-319-707	Sequence 707, App	
7	344.2	66.6	7260	13	US-09-960-706-1066	Sequence 1066, Ap	
8	344.2	66.6	7260	15	US-10-136-639-4	Sequence 4, Appli	
9	342.6	66.3	725	15	US-10-207-655-54	Sequence 54, Appli	
10	325.2	62.9	539	9	US-09-852-261-3	Sequence 3, Appli	
11	318.2	61.5	651	15	US-10-161-088-1	Sequence 1, Appli	
12	285.4	55.2	612	13	US-10-251-661-7	Sequence 7, Appli	
13	258.4	50.0	318	9	US-09-852-261-9	Sequence 9, Appli	
14	247.8	47.9	487	9	US-09-852-261-11	Sequence 11, Appli	
15	228	44.1	462	15	US-10-238-114-1	Sequence 1, Appli	
16	210	40.6	210	13	US-09-807-742-18	Sequence 18, Appli	
17	208.4	40.3	2862	13	US-10-241-596-13	Sequence 13, Appli	
18	204.6	39.6	4532	10	US-09-930-377B-1	Sequence 1, Appli	
19	203.6	39.4	210	10	US-09-930-377B-2	Sequence 2, Appli	
20	202.8	39.2	390	15	US-10-179-046-13	Sequence 13, Appli	
21	202	39.1	286	15	US-10-161-088-3	Sequence 3, Appli	
22	183	35.4	516	13	US-10-029-386-5832	Sequence 5832, Ap	
23	182	35.2	182	13	US-10-029-386-18231	Sequence 18231, A	
24	140.2	27.1	213	15	US-10-076-816-9	Sequence 9, Appli	
25	140.2	27.1	213	15	US-10-077-381-9	Sequence 9, Appli	
26	123.8	23.9	621	9	US-09-921-398-40	Sequence 40, Appli	
27	123.8	23.9	621	15	US-10-280-826-40	Sequence 40, Appli	
28	108.6	21.0	480	9	US-09-921-398-38	Sequence 38, Appli	
29	108.6	21.0	480	15	US-10-280-826-38	Sequence 38, Appli	
30	101.2	19.6	210	13	US-09-807-742-19	Sequence 19, Appli	
31	75.4	14.6	411	10	US-09-960-352-2082	Sequence 2082, Ap	
32	72.4	14.0	854	10	US-09-954-531-989	Sequence 989, App	
33	71.8	13.9	237	15	US-10-136-841-3	Sequence 3, Appli	
C	34	70.6	13.7	447	9	US-09-922-217-917	Sequence 917, App
C	35	70.6	13.7	447	10	US-09-833-263-917	Sequence 917, App
C	36	70.6	13.7	447	14	US-10-025-380-917	Sequence 917, App
C	37	70.4	13.6	437	15	US-10-066-543-663	Sequence 663, App
C	38	70.4	13.6	493	15	US-10-066-543-997	Sequence 997, App
C	39	70.4	13.6	518	15	US-10-066-543-1040	Sequence 1040, Ap
C	40	70.4	13.6	536	15	US-10-066-543-428	Sequence 428, App
41	70.4	13.6	543	15	US-10-136-841-1	Sequence 1, Appli	
C	42	70.4	13.6	549	15	US-10-066-543-478	Sequence 478, App
C	43	70.4	13.6	574	9	US-09-922-217-918	Sequence 918, App
C	44	70.4	13.6	574	10	US-09-833-263-918	Sequence 918, App
C	45	70.4	13.6	574	14	US-10-025-380-918	Sequence 918, App

ALIGNMENTS

RESULT 1

US-09-852-261-1

; Sequence 1, Application US/09852261

; Patent No. US20020083477A1

; GENERAL INFORMATION:

; APPLICANT: GOLDSPIK, GEOFFREY

; APPLICANT: TERENGHI, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-852-261-1

Query Match 100.0%; Score 517; DB 9; Length 517;
Best Local Similarity 100.0%; Pred. No. 2.4e-160;
Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC 60
|||
Db 1 GGACCGGAGACGCTCTGGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC 60

Qy 61 AGGGGTTTTATTCAACAAGCCCACAGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG 120
|||
Db 61 AGGGGTTTTATTCAACAAGCCCACAGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG 120

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
|||
Db 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy 181 TGGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGGCCAACCGAC 240
|||
Db 181 TGGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGGCCAACCGAC 240

Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
|||
Db 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300

Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAACAAGAACTACAG 360
|||
Db 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAACAAGAACTACAG 360

Qy 361 GATGTAGAACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTCT 420
|||
Db 361 GATGTAGAACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTCT 420

Qy 421 GCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTCAAA 480
|||
Db 421 GCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTCAAA 480

Qy 481 GATGGCATTTCCCCAATGAAATACACAAGTAAACAT 517
|||
Db 481 GATGGCATTTCCCCAATGAAATACACAAGTAAACAT 517

RESULT 2

US-09-852-261-5

; Sequence 5, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPINK, GEOFFREY
; APPLICANT: TERENGHI, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus

US-09-852-261-5

Query Match 90.4%; Score 467.4; DB 9; Length 523;
Best Local Similarity 96.2%; Pred. No. 6.1e-144;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGCCGGCTGAGCTGGTGGATGCTCTTCAGTTCTGTGTGGAGAC 60
Db 1 GGACCGGAGACGCTCTGCCGGCTGAGCTGGTGGATGCTCTTCAGTTCTGTGTGGAGAC 60

Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
Db 61 AGGGGCTTTATTCAACAAGCCCACAGGATACTGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
Db 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGGCCAACACCGAC 240
Db 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGGCCGCTCCGTGCCAGGCCAACACCGAC 240

Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
Db 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAATGAAGTCTCAGAGG 300

Qy 298 AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
Db 301 AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy 358 CAGGATGTA-GAAGACCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 416
Db 361 CAGGATGTTAGGAAGACCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 420

Qy 417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATT 476
Db 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATT 480

Qy 477 CAAAGATGGCATTCCCCAATGAAATACACAAGTAAACAT 517

Qy	420	TGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTCAA	479
Db	372	TGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTCAA	431
Qy	480	AGATGGCATTCCCCAATGAAATACACAAGTAAACAT	517
Db	432	AGATGGCATTCCCCAATGAAATACACAAGTAAACAT	469

RESULT 4

US-09-919-497-24

; Sequence 24, Application US/09919497

; Patent No. US20020106662A1

; GENERAL INFORMATION:

; APPLICANT: Mutter, George L.

; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER

; FILE REFERENCE: B0801/7225

; CURRENT APPLICATION NUMBER: US/09/919,497

; CURRENT FILING DATE: 2001-07-31

; PRIOR APPLICATION NUMBER: US 60/221,735

; PRIOR FILING DATE: 2000-07-31

; NUMBER OF SEQ ID NOS: 100

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 24

; LENGTH: 7260

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-919-497-24

Query Match 66.6%; Score 344.2; DB 10; Length 7260;
 Best Local Similarity 87.3%; Pred. No. 1.3e-102;
 Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy	1	GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTTCAGTTCTGTGTGGAGAC	60
Db	311	GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTTCAGTTCTGTGTGGAGAC	370
Qy	61	AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG	120
Db	371	AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG	430
Qy	121	ACAGGCATCGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	431	ACAGGCATCGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	490
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCTGCCAGCGCCACACCGAC	240
Db	491	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCTGCCAGCGCCACACCGAC	550
Qy	241	ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA	300
Db	551	ATGCCCAAGACCCAG-----	565

Qy	301	AGGAAAGGAAGTACATTGAAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	360
Db	566	---AAGGAAGTACATTGAAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	621

Qy	361	GATGTA-GAAGACCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC	419
Db	622	GATGTAGGAAGACCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC	681
Qy	420	TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC	477
Db	682	TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTAA	741
Qy	478	AAAGAT-GGCATTTCCCCAATGAAATACACAAGTAAACAT	517
Db	742	AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT	782

RESULT 5

US-09-880-107-3739

; Sequence 3739, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3739
; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X57025

US-09-880-107-3739

Query Match 66.6%; Score 344.2; DB 10; Length 7260;
Best Local Similarity 87.3%; Pred. No. 1.3e-102;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy	1	GGACCGGAGACGCTCTGGGGCTGAGCTGGATGCTTCAGTCGTGTGGAGAC	60
Db	311	GGACCGGAGACGCTCTGGGGCTGAGCTGGATGCTTCAGTCGTGTGGAGAC	370
Qy	61	AGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG	120
Db	371	AGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG	430
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	431	ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	490
Qy	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240

```

Db      ||||||| 491 TCGGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGGCCACACCGAC 550
Qy      241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
Db      ||||||| 551 ATGCCCAAGACCCAG----- 565
Qy      301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
Db      566 ----AAGGAAGTACATTGAAGAACCGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 621
Qy      361 GATGTA-GAACACCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC 419
Db      622 GATGTAGGAAGACCCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC 681
Qy      420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGCCAAAAATAAGTTGATCACATTTC 477
Db      682 TGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTGATAACATTAA 741
Qy      478 AAAGAT-GGCATTCCCCAATGAAATACACAAGTAAACAT 517
Db      ||||||| 742 AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT 782

```

RESULT 6

US-09-873-319-707

; Sequence 707, Application US/09873319A
; Publication No. US20030134324A1
; GENERAL INFORMATION:
; APPLICANT: Munger, William E.
; APPLICANT: Kulkarni, Prakash
; APPLICANT: Getzenberg, Robert H.
; APPLICANT: Waga, Iwao
; APPLICANT: Yamamoto, Jun
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
; TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles
; FILE REFERENCE: 44921-5029-US
; CURRENT APPLICATION NUMBER: US/09/873,319A
; CURRENT FILING DATE: 2001-06-05
; EARLIER APPLICATION NUMBER: US 60/223,323
; EARLIER FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 755
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 707
; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134324A1 X57025

US-09-873-319-707

Query Match 66.6%; Score 344.2; DB 13; Length 7260;
Best Local Similarity 87.3%; Pred. No. 1.3e-102;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTTCAGTTCTGAGAC 60
|||||||

Db 311 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC 370
 Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
 |||||
 Db 371 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430
 |||||
 Qy 121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
 |||||
 Db 431 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490
 |||||
 Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCAACCGAC 240
 |||||
 Db 491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCAACCGAC 550
 |||||
 Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
 |||||
 Db 551 ATGCCCAAGACCCAG----- 565
 |||||
 Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
 |||||
 Db 566 ---AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 621
 |||||
 Qy 361 GATGTA-GAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTGCTC 419
 |||||
 Db 622 GATGTAGGAAGACCCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC 681
 |||||
 Qy 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC 477
 |||||
 Db 682 TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTTC 741
 |||||
 Qy 478 AAAGAT-GGCATTCCCCAATGAAATACACAAGTAAACAT 517
 |||||
 Db 742 AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT 782

RESULT 7

US-09-960-706-1066

; Sequence 1066, Application US/09960706
 ; Publication No. US20030134280A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Munger, William E.
 ; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia Using
 ; TITLE OF INVENTION: Gene Expression Profiles
 ; FILE REFERENCE: 44921-5029-01US
 ; CURRENT APPLICATION NUMBER: US/09/960,706
 ; CURRENT FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: 60/223,323
 ; PRIOR FILING DATE: 2000-08-07
 ; PRIOR APPLICATION NUMBER: 09/873,319
 ; PRIOR FILING DATE: 2001-06-05
 ; NUMBER OF SEQ ID NOS: 1124
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1066
 ; LENGTH: 7260
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Genbank Accession No. US20030134280A1 X57025
US-09-960-706-1066

Query Match 66.6%; Score 344.2; DB 13; Length 7260;
Best Local Similarity 87.3%; Pred. No. 1.3e-102;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy 1 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGATGCTCTCAGTCGTGTGGAGAC 60
|||
Db 311 GGACCGGAGACGCTCTGCAGGGCTGAGCTGGATGCTCTCAGTCGTGTGGAGAC 370
|||
Qy 61 AGGGGCTTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCCCTCAG 120
|||
Db 371 AGGGGCTTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCCCTCAG 430
|||
Qy 121 ACAGGCATCGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
|||
Db 431 ACAGGCATCGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490
|||
Qy 181 TCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
|||
Db 491 TCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550
|||
Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
|||
Db 551 ATGCCCAAGACCCAG----- 565
|||
Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
|||
Db 566 ---AAGGAAGTACATTGAAGAACCGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 621
|||
Qy 361 GATGTA-GAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC 419
|||
Db 622 GATGTAGGAAGACCCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC 681
|||
Qy 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC 477
|||
Db 682 TGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTGATAACATTTC 741
|||
Qy 478 AAAGAT-GGCATTCCCCAATGAAATACACAAGTAAACAT 517
|||
Db 742 AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT 782

RESULT 8

US-10-136-639-4

; Sequence 4, Application US/10136639

; Publication No. US20030072761A1

; GENERAL INFORMATION:

; APPLICANT: LeBowitz, Jonathan

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TARGETING PROTEINS ACROSS THE BLOOD BRAIN

; TITLE OF INVENTION: BARRIER

; FILE REFERENCE: SYM-008

; CURRENT APPLICATION NUMBER: US/10/136,639

; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: US 60/329,650
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-136-639-4

Query Match 66.6%; Score 344.2; DB 15; Length 7260;
Best Local Similarity 87.3%; Pred. No. 1.3e-102;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy 1 GGACCGGAGACGCTCTGCCGGCTGAGCTGGATGCTCTCAGTTCTGTGTGGAGAC 60
|||
Db 311 GGACCGGAGACGCTCTGCCGGCTGAGCTGGATGCTCTCAGTTCTGTGTGGAGAC 370

Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
|||
Db 371 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
|||
Db 431 ACAGGCATCGTGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGCCGTGCCAGCGCCACACCGAC 240
|||
Db 491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGCCGTGCCAGCGCCACACCGAC 550

Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
|||
Db 551 ATGCCCAAGACCCAG----- 565

Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
|||
Db 566 ----AAGGAAGTACATTGAAGAACCGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 621

Qy 361 GATGTA-GAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTGCTC 419
|||
Db 622 GATGTAGGAAGACCCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC 681

Qy 420 TGCAC-AGTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC 477
|||
Db 682 TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTAA 741

Qy 478 AAAGAT-GGCATTCCCCAATGAAATACACAAGTAAACAT 517
|||
Db 742 AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT 782

RESULT 9

US-10-207-655-54

; Sequence 54, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.

; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; LENGTH: 725
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-207-655-54

Query Match 66.3%; Score 342.6; DB 15; Length 725;
Best Local Similarity 87.1%; Pred. No. 1.4e-102;
Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;

Qy 1 GGACCGGAGACGCTCTGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGAC 60
Db 156 GGACCGGAGACGCTCTGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGAC 215

Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
Db 216 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 275

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
Db 276 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 335

Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
Db 336 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 395

Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
Db 396 ATGCCCAAGACCCAG----- 410

Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 360
Db 411 ---AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG 466

Qy 361 GATGTA-GAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTGCTC 419
Db 467 GATGTAGGAAGACCCCTCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTGCTC 526

Qy 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTGATCACATTTC 477
Db 527 TGCACGAGTTACCTGTTAAACTTGGAACACCTACCAAAAAATAAGTTGATAACATTAA 586

Qy 478 AAAGAT-GGCATTTCCCCAATGAAATACACAAGTAAACAT 517
Db 587 AAAGATGGCGTTCCCCAATGAAATACACAAGTAAACAT 627

RESULT 10
US-09-852-261-3
; Sequence 3, Application US/09852261

; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPIK, GEOFFREY
; APPLICANT: TERENGHI, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 539
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-852-261-3

Query Match 62.9%; Score 325.2; DB 9; Length 539;
Best Local Similarity 81.2%; Pred. No. 6.8e-97;
Matches 429; Conservative 0; Mismatches 88; Indels 11; Gaps 4;

Qy 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTTCAGTTCGTGTGGAGAC 60
Db ||||| ||||| ||| ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCCCTCAG 120
Db 61 AGGGGCTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTGGAGGGACCACAG 120
Qy 121 ACAGGCATCGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
Db 121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Qy 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGGCCACACCGAC 240
Db 181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTCCATCCGGGCCAGGCCACACTGAC 240
Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
Db 241 ATGCCCAAGACTCAGAAGTCCCAGCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
Qy 298 AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
Db 301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
Qy 358 CAGGATGTA-GAAGACCCCTCTGAGGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 416
Db 361 CAGAATGTAGGAGGAGCCTCCGAGGAACAGAAAATGCCACGTACCGCAAGATCCTTTG 420
Qy 417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTGATC 470
Db 421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAATATCAATAATGAGTTCAATA 480
Qy 471 ACATTTCAAAGAT-GGCATTTCCCCAATGAAATACACAAGTAAACAT 517
Db 481 TCATTTCAGAGATGGCATTCCCTCAATGAAATACACAAGTAAACAT 528

RESULT 11

US-10-161-088-1

; Sequence 1, Application US/10161088
; Publication No. US20030077761A1
; GENERAL INFORMATION:
; APPLICANT: Parrow, Vendela
; APPLICANT: Rosengren, Linda
; TITLE OF INVENTION: NEW METHODS
; FILE REFERENCE: 13425-111001
; CURRENT APPLICATION NUMBER: US/10/161,088
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: SE 0101934-8
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73) ... (471)

US-10-161-088-1

Query Match 61.5%; Score 318.2; DB 15; Length 651;
Best Local Similarity 81.7%; Pred. No. 1.5e-94;
Matches 419; Conservative 0; Mismatches 83; Indels 11; Gaps 4;

Qy 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC 60
Db 139 GGACCAGAGACCCCTTGCGGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGACCG 198

Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 120
Db 199 AGGGGCTTTACTCAACAAGCCCACAGGCTATGGCTCCAGCATTGGAGGGCACCTCAG 258

Qy 121 ACAGGCATCGTGGATGAGTGTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
Db 259 ACAGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 318

Qy 181 TGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGGCCAACCCGAC 240
Db 319 TGTGCCCACTGAAGCCTACAAAGCAGCCGCTCTATCCGTGCCAGCGCCACACTGAC 378

Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
Db 379 ATGCCCAAGACTCAGAAGTCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 438

Qy 298 AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
Db 439 AGAAGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 498

Qy 358 CAGGATGTA-GAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 416
Db 499 CAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTG 558

Qy 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA 300
 |||||
 Db 487 ATGCCCAAGACCCAG----- 501
 |||||
 Qy 301 AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGAGGAAACAAGAACTACAG 360
 |||||
 Db 502 ---AAGGAAGTACATTGAAGAACGCAAGTAGAGGGAGTGAGGAAACAAGAACTACAG 557
 |||||
 Qy 361 GATGTA-GAAGACCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCC 414
 |||||
 Db 558 GATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTT 612

RESULT 13

US-09-852-261-9

; Sequence 9, Application US/09852261
 ; Patent No. US20020083477A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GOLDSPIK, GEOFFREY
 ; APPLICANT: TERENGHI, GIORGIO
 ; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
 ; FILE REFERENCE: 117-351
 ; CURRENT APPLICATION NUMBER: US/09/852,261
 ; CURRENT FILING DATE: 2001-05-10
 ; PRIOR APPLICATION NUMBER: GB 0011278.9
 ; PRIOR FILING DATE: 2000-05-10
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 318
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-852-261-9

Query Match 50.0%; Score 258.4; DB 9; Length 318;
 Best Local Similarity 99.6%; Pred. No. 6.6e-75;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGGGGCTGAGCTGGATGCTTCAGTCGTGTGGAGAC 60
 |||||
 Db 1 GGACCGGAGACGCTCTGGGGCTGAGCTGGATGCTTCAGTCGTGTGGAGAC 60
 |||||
 Qy 61 AGGGCTTTATTCACACAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 120
 |||||
 Db 61 AGGGCTTTATTCACACAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 120
 |||||
 Qy 121 ACAGGCATCGTGGATGAGTGTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
 |||||
 Db 121 ACAGGCATCGTGGATGAGTGTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
 |||||
 Qy 181 TGCGCACCCCTCAAGCCTGCCAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
 |||||
 Db 181 TGCGCACCCCTCAAGCCTGCCAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240
 |||||
 Qy 241 ATGCCCAAGACCCAGAAGTA 260
 |||||
 Db 241 ATGCCCAAGACCCAGAAGGA 260

RESULT 14

US-09-852-261-11

; Sequence 11, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPIK, GEOFFREY
; APPLICANT: TERENGHI, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Rattus sp.

US-09-852-261-11

Query Match 47.9%; Score 247.8; DB 9; Length 487;
Best Local Similarity 74.5%; Pred. No. 2.6e-71;
Matches 391; Conservative 0; Mismatches 77; Indels 57; Gaps 4;

Qy	1	GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTCTTCAGTTCTGTGTGGAGAC	60
Db	1	GGACCAAGAGACCCTTGCGGGCTGAGCTGGTGGACGCTCTTCAGTTCTGTGTGGACCA	60
Qy	61	AGGGGCTTTTATTCAACAAGCCCACAGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	120
Db	61	AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTGGAGGGCACACAG	120
Qy	121	ACAGGCATCGGATGAGTGCTGCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Db	121	ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Qy	181	TGCCACCCCTCAAGCCTGCCAACGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240
Db	181	TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTCCATCGGGCCAGCGCCACACTGAC	240
Qy	241	ATGCCCAAGACCCAGAACAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCAGAGA	300
Db	241	ATGCCCAAGACTCAG-----	255
Qy	301	AGGAAAGGAAGTACATTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAG	360
Db	256	---AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTACAG	311
Qy	361	GATGTA-GAAGACCCCTCTGAGGAGTGAAGAACAGGCCACCGCAGGACCCCTTGCTC	419
Db	312	AATGTAGGAGGAGCCTCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTGCTG	371
Qy	420	TGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTGATCACA	473

Db 372 CTTGAGCAACCTGCAAAACATCGAACACCTGCCAATATCAATAATGAGTTCAATATCA 431
Qy 474 TTTCAAAGAT-GGCATTCCCCAATGAAATACACAAGTAAACAT 517
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 432 TTTCAGAGATGGCATTCCCTCAATGAAATACACAAGTAAACAT 476

RESULT 15

US-10-238-114-1

; Sequence 1, Application US/10238114
; Publication No. US20030100073A1
; GENERAL INFORMATION:
; APPLICANT: Merial
; APPLICANT: ANDREONI , Christine Michele
; TITLE OF INVENTION: IGF-1 AS FELINE VACCINE ADJUVANT, IN PARTICULAR AGAINST
FELINE RETROVIRUS
; FILE REFERENCE: 454313-3165.1
; CURRENT APPLICATION NUMBER: US/10/238,114
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: FR 01 11736
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/318,666
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Felis catus
US-10-238-114-1

Query Match 44.1%; Score 228; DB 15; Length 462;
Best Local Similarity 92.3%; Pred. No. 9e-65;
Matches 240; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Qy 1 GGACCGGAGACGCTCTGCGGGCTGAGCTGGTGGATGCTTCAGTCGTGTGGAGAC 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 145 GGACCAGAGACGCTCTGCGGGCTGAGTTGGTGGACGCTTCAGTCGTGTGGAGAC 204
Qy 61 AGGGGCTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 205 AGGGGTTTTATTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCACCTCAG 264
Qy 121 ACAGGCATCGGGATGAGTGTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 265 ACAGGCATCGGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGGCGTAGAGATGTAC 324
Qy 181 TGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCTGCCAGCGCCACACCGAC 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 325 TGTGCACCCCTCAAGCCTGCCAAGTCAGCTGCCGCTCAGTCGTGCTCAGCGCCACACTGAC 384
Qy 241 ATGCCCAAGACCCAGAAGTA 260
||| ||| ||| ||| |||
Db 385 ATGCCCAAGGCTCAGAAGGA 404

Search completed: December 13, 2003, 11:56:45

Job time : 232.833 secs